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(54) Non-reducing saccharide-forming enzyme, DNA encoding it, and their preparations and uses.

(57) A DNA encoding an enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from amylaceous saccharides having a degree of glucose polymerization of 3 or higher, enables an industrial-scale production of a recombinant enzyme with such enzyme activity. Non-reducing saccharides obtainable by the recombinant enzyme can be used in a variety of food products, cosmetics, pharmaceuticals and feeds because of their substantial non-reducibility, mild and high-quality sweetness, adequate viscosity, and moisture-retaining ability.

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The present invention relates to a novel DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher, and a recombinant DNA and enzyme containing the DNA as well as to a transformant. The present invention further relates to preparations and uses thereof.

5 Trehalose is a disaccharide which consists of 2 glucose molecules that are linked together with their reducing groups, and, naturally, it is present in fungi, algae, insects, etc., in an extremely small quantity. Having no reducing residue within the molecule, trehalose does not cause an unsatisfactory browning reaction even when heated in the presence of amino acids or the like, and because of this it can sweeten food products without fear of causing unsatisfiable coloration and deterioration. Trehalose, however, is far from being readily prepared in a desired amount by conventional production methods, and, actually, it has not scarcely been used for sweetening food products.

10 Conventional production methods are roughly classified into 2 groups, i.e. the one using cells of microorganisms and the other employing a multi-enzymatic system wherein enzymes are allowed to act on saccharides. The former, as disclosed in Japanese Patent Laid-Open No.154,485/75, is a method comprising growing microorganisms such as bacteria and yeasts in nutrient culture media, and collecting trehalose from the proliferated cells in the resultant cultures. The latter, as disclosed in Japanese Patent Laid-Open No.216,695/83, is a method comprising providing maltose as a substrate, allowing a multi-enzymatic system using maltose- and trehalose-phosphorylases to act on maltose, and recovering the formed trehalose from the reaction system. Although the former facilitates to grow microorganisms with a relative easiness, it requires sequential complicated steps for collecting trehalose from the microorganisms containing only 15 w/w % trehalose, on a dry solid basis (d.s.b.). While the latter enables to separate trehalose with a relative easiness, but it is theoretically difficult to increase the trehalose yield by allowing enzymes to act on substrates at a considerably-high concentration because the enzymatic reaction in itself is an equilibrium reaction of 2 different types of enzymes and the equilibrium point constantly inclines to the side of forming glucose phosphate.

15 25 In view of the foregoing, the present inventors energetically screened enzymes which form saccharides having trehalose structure from amyloseous saccharides, and found that microorganisms such as those of the splices *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 produce a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher. Before or after this finding, it was revealed that such a non-reducing saccharide is almost quantitatively hydrolyzed into trehalose and glucose and/or maltooligosaccharides by another enzyme produced by the same microorganisms as mentioned above. Since the combination use of the enzymes enables to form a desired amount of trehalose with a relative easiness, the aforementioned objects relating to trehalose would be completely overcome. Insufficient producibility of the novel enzyme by such a microorganism results in a drawback, i.e. a relatively-large scale culture thereof is inevitable to industrially produce trehalose and/or non-reducing saccharides having trehalose structure as an end unit.

20 30 35 Recombinant DNA technology has made a remarkable progress in recent years. At present, even an enzyme whose total amino acid sequence has not been revealed can be readily prepared in a desired amount, if a gene encoding the enzyme was once isolated and the base sequence was decoded, by preparing a recombinant DNA which contains a DNA encoding the enzyme, introducing the recombinant DNA into microorganisms or cells of plants and animals, and culturing the resultant transformants. Under the background, urgently required are to find a gene encoding the enzyme and to reveal a base sequence thereof.

40 It is an aim of the present invention to provide a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher.

45 It is a further aim of the present invention to provide a recombinant DNA which contains the DNA and a self-replicable vector.

It is yet another aim of the present invention to provide a recombinant enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher, by means of recombinant DNA technology.

50 It is another aim of the present invention to provide a transformant obtainable by introducing the recombinant DNA into a suitable host.

It is a further aim of the present invention to provide a preparation of the recombinant enzyme.

It is yet another aim of the present invention to provide a method to convert reducing amyloseous saccharides by using the recombinant enzyme.

55 The present invention provides a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher.

The present invention further provides a replicable recombinant DNA which contains a self-replicable vec-

tor and a DNA which encodes a non-reducing saccharide-forming enzyme.

The present invention further provides a recombinant enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher.

5 The present invention further provides a transformant into which a replicable recombinant DNA containing a self-replicable vector and a DNA encoding an enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher.

10 The present invention further provides a process for producing a recombinant enzyme, which contains a step of culturing a transformant capable of forming the recombinant enzyme, and collecting the enzyme from the resultant culture.

15 The present invention further provides a method for converting reducing amyloseous saccharides, which contains a step of allowing the recombinant enzyme to act on reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher to form from them non-reducing saccharides having trehalose structure as an end unit.

The invention will now be described in further detail, by way of example only, with reference to the accompanying drawings, in which:

FIG. 1 shows the optimum temperature of enzyme M-11.

FIG. 2 shows the optimum temperature of enzyme Q36.

20 FIG. 3 shows the optimum pH of enzyme M-11.

FIG. 4 shows the optimum pH of enzyme Q36.

FIG. 5 shows the thermal stability of enzyme M-11.

FIG. 6 shows the thermal stability of enzyme Q36.

FIG. 7 shows the pH stability of enzyme M-11.

25 FIG. 8 shows the pH stability of enzyme Q36.

FIG. 9 is a restriction map of the recombinant DNA pBMT7 according to the present invention. In the figure, a bold-lined part shows a DNA encoding enzyme M-11.

FIG. 10 is a restriction map of the recombinant DNA pBQT13 according to the present invention. In the figure, a bold-lined part shows a DNA encoding enzyme Q36.

30 The DNA according to the present invention exerts the production of the non-reducing saccharide-forming enzyme encoded by the DNA in a manner that the DNA is inserted into an appropriate self-replicable vector to form a replicable recombinant DNA, followed by introducing the recombinant DNA into a host, which is incapable of producing the enzyme but readily replicable, to form a transformant.

35 Although the recombinant DNA *per se* does not produce the enzyme, the production of the enzyme encoded by the DNA is induced by introducing the recombinant DNA into a host, which is incapable of producing the enzyme but replicable with a relative easiness, to form a transformant, and culturing the transformant to produce the enzyme.

The transformant according to the present invention produces the enzyme when cultured.

The recombinant enzyme according to the present invention acts on reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher to form non-reducing saccharides having trehalose structure as an end unit.

The culture of the transformant according to the present invention yields a desired amount of the enzyme with a relative easiness.

40 The conversion method according to the present invention converts reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher into non-reducing saccharides having trehalose structure as an end unit.

45 The present invention was made based on the finding of a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher. The enzyme can be obtained from cultures of microorganisms of the species *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 (the enzymes from *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 are respectively designated as "enzyme M-11" and "enzyme Q36" hereinafter), and the present inventors isolated the enzyme by the combination use of conventional purification methods using column chromatography mainly, and examined the properties and features to reveal the reality, i.e. a polypeptide having the following physicochemical properties:

50 (1) Action

Forming non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher;

(2) Molecular weight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE);

(3) Isoelectric point

About 3.6-4.6 on isoelectrophoresis;

(4) Optimum temperature

5 Exhibiting an optimum temperature of around 35-40°C when incubated at pH 7.0 for 60 min;

(5) Optimum pH

Exhibiting an optimum pH of around 6.4-7.2 when incubated at 40°C for 60 min;

(6) Thermal stability

Stable up to a temperature of around 35-40°C when incubated at pH 7.0 for 60 min; and

10 (7) pH Stability

Stable up to a pH of around 5.5-11.0 when incubated at 25°C for 16 hours.

The experiments, which were conducted to reveal the aforesaid physicochemical properties, are explained in the below:

15 Experiment 1

Preparation of purified enzyme

Experiment 1-1

Preparation of enzyme derived from *Rhizobium* sp. M-11

In 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid culture medium (pH 7.0) containing 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate, and 25 0.1 w/v % potassium dihydrogen phosphate, and the flasks were autoclaved at 120°C for 20 min to effect sterilization. After cooling the flasks a seed culture of *Rhizobium* sp. M-11 was inoculated into each liquid culture medium in each flask, followed by the incubation at 27°C for 24 hours under rotary-shaking conditions. Twenty L of a fresh preparation of the same liquid culture medium was put in a 30-L jar fermentor and sterilized, followed by inoculating one v/v % of the culture obtained in the above into the sterilized liquid culture medium in the jar 30 fermentor, and incubating it at a pH of 6-8 and 30°C for 24 hours under aeration and agitation conditions.

Thereafter, about 18 L of the resultant culture was subjected to an ultra-high pressure cell disrupting apparatus to disrupt cells, and the resultant suspension was centrifuged to obtain a supernatant, and to about 16 L of which was added ammonium sulfate to give a 20 w/v % saturation, allowed to stand at 4°C for one hour, and centrifuged to remove sediment. To the resultant supernatant was added ammonium sulfate to give 35 a 60 w/v % saturation, allowed to stand at 4°C for 24 hours, and centrifuged to collect sediment which was then dissolved in a minimum amount of 10 mM phosphate buffer (pH 7.0). The resultant solution was dialyzed against 10 mM phosphate buffer (pH 7.0) for 24 hours, and centrifuged to remove insoluble substances. The supernatant thus obtained was fed to a column packed with "DEAE-TOYOPEARL®", a product for ion-exchange chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 10 mM phosphate buffer (pH 7.0), followed by feeding to the column a linear gradient buffer of 40 sodium chloride ranging from 0 M to 0.5 M in 10 mM phosphate buffer (pH 7.0). Fractions containing the objective enzyme were collected from the eluate, pooled, dialyzed for 10 hours against 50 mM phosphate buffer (pH 7.0) containing 2 M ammonium sulfate, and centrifuged to remove insoluble substances. Thereafter, the resultant supernatant was fed to a column, which had been packed with "BUTYL TOYOPEARL®", a gel for 45 hydrophobic column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, and equilibrated with 50 mM phosphate buffer (pH 7.0) containing 2 M ammonium sulfate, followed by feeding to the column a linear gradient buffer of ammonium sulfate ranging from 2 M to 0 M in 50 mM phosphate buffer (pH 7.0). Fractions containing the objective enzyme were collected from the eluate, pooled, fed to a column packed with "TOYOPEARL® HW-55", a product for gel filtration chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 50 mM phosphate buffer (pH 7.0), followed by feeding to the column 50 mM phosphate buffer (pH 7.0) and collecting fractions containing the objective enzyme. The enzyme thus obtained had a specific activity of about 195 units/mg protein, and the yield was 50 about 220 units per L of the culture.

Throughout the specification the enzyme activity is expressed by the value measured on the following assay: Place 4 ml of 50 mM phosphate buffer (pH 7.0) containing 1.25 w/v % maltopentaose in a test tube, add one ml of an enzyme solution to the tube, and incubate the resultant solution at 40°C for 60 min to effect enzymatic reaction. Thereafter, heat the resultant reaction mixture at 100°C for 10 min to suspend the enzymatic reaction. Dilute the resultant reaction mixture with distilled water by 10 times, and assay the reducing activity

on the Somogyi-Nelson's method. One unit activity of the enzyme is defined as the amount of enzyme which reduces the reducing power corresponding to one μmol maltopentaose per min under the same conditions as described above.

5 Experiment 1-2

Purification of enzyme Q36

10 Similarly as in Experiment 1-1, a seed culture of *Arthrobacter* sp.Q36 was cultured, and the resultant culture was treated to obtain a purified enzyme Q36 having a specific activity of about 200 units/mg protein in a yield of about 295 units per L of the culture.

Experiment 2

15 Physicochemical property of enzyme

Experiment 2-1

Action

20 To 50 mM phosphate buffer (pH 7.0) containing 20 w/v % of glucose, maltose, maltotriose, maltotetraose, maltopentaose, maltohexaose or maltoheptaose as a substrate was added 2 units/g substrate, d.s.b., of the purified enzyme M-11 or enzyme Q36 obtained in Experiment 1, and the mixture was enzymatically reacted at 40°C for 48 hours. The reaction mixture was desalted in usual manner, fed to "WB-T-330", a column for high-performance liquid chromatography (HPLC) commercialized by Tosoh Corporation, Tokyo, Japan, followed by feeding to the column distilled water at a flow rate of 0.5 ml/min at ambient temperature to separate saccharides contained in the reaction mixture while monitoring the saccharide concentration of the eluate with "MODEL RI-8012", a differential refractometer commercialized by Wako Pure Chemical Industries, Ltd., Tokyo, Japan. The saccharide composition of the reaction mixture was given in Table 1 or 2. In the table, the symbols "P1" to "P5" were named for the formed saccharides in the order from the smallest one to the largest one in terms of their degrees of glucose polymerization.

Table 1

	Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
35	Glucose	Glucose	33.4	100.0
	Maltose	Maltose	28.5	100.0
40	Maltotriose	P1 + Maltotriose	23.3 25.9	35.0 65.0
	Maltotetraose	P2 + Maltotetraose	21.6 24.1	85.6 14.4
45	Maltopentaose	P3 + Maltopentaose	19.7 22.6	92.7 7.3
	Maltohexaose	p4 + Maltohexaose	18.7 21.4	93.5 6.5
50	Maltoheptaose	P5 + Maltoheptaose	17.8 21.0	93.4 6.7
55				

Table 2

5	Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
	Glucose	Glucose	33.4	100.0
10	Maltose	Maltose	28.5	100.0
	Maltotriose	P1 + Maltotriose	23.3 25.9	35.5 64.5
15	Maltotetraose	P2 + Maltotetraose	21.6 24.1	85.8 14.2

20 (Continued)

	Substrate	Saccharide in reaction mixture	Elution time (min)	Composition (%)
25	Maltopentaose	P3 + Maltopentaose	19.7 22.6	92.9 7.1
	Maltohexaose	P4 + Maltohexaose	18.7 21.4	93.2 6.7
30	Maltoheptaose	P5 + Maltoheptaose	17.8 21.0	93.1 6.9

35 As is evident from the results in Table 1 and 2, the enzymes M-11 and Q36 newly formed saccharides from reducing saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose, but not from those having a degree of glucose polymerization less than 3 such as glucose and maltose. In the enzymatic reaction, the newly formed saccharides were P1 to P5, and the total yield of the saccharides P2 to P5 was as high as 85 w/w % or more, d.s.b.

40 To separate the saccharides P1 to P5, 3 jacketed stainless steel columns, having an inner diameter of 2.0 cm and a length of one m, were packed with "XT-1016, Na⁺", a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, and cascaded in series. The reaction mixture containing any one of saccharides P1 to P5 was separatory applied to the columns at an inner column temperature of 55°C, followed by applying to the columns with 55°C distilled water at a flow rate of SV (space velocity) 0.13. After examining the saccharide composition of the resultant eluate, a fraction containing 97 w/w or more, d.s.b., of any one of saccharides P1 to P5 was recovered and pulverized in vacuo. No substantial reducing power was detected in the purified saccharides P1 to P5 on the Somogyi-Nelson's method.

45 To identify the saccharides P1 to P5, 50 mg one of which was weighed, dissolved in one ml of 50 mM acetate buffer (pH 4.5), and mixed with one unit of glucoamylase, followed by incubating the mixture at 40°C for 6 hours. High-performance liquid chromatography analysis on the resultant reaction mixture detected glucose and trehalose as shown in Tables 3 and 4. When the saccharides P1 to P5 were subjected to the action of β-amylase, the saccharides P1 and P2 were not hydrolyzed by β-amylase, but the saccharides P3, P4 and P5 were respectively hydrolyzed into one mole of maltose, P2 and one mole of maltose, and P1 and 2 moles of maltose.

Table 3

5	Substrate	Glucose (%)	Trehalose (%)	Molar ratio*
	P1	36.2	63.8	1.07
10	P2	52.0	48.0	2.06
	P3	61.4	38.6	3.02
15	P4	68.3	31.7	4.09
	P5	72.9	27.1	5.11

20 Note: The molar ratios as indicated with the symbol "*" are values calculated as moles of glucose against one mole of trehalose.

Table 4

25	Substrate	Glucose (%)	Trehalose (%)	Molar ratio
	P1	36.0	64.0	1.07
30	P2	51.5	48.5	2.02
	P3	61.6	38.4	3.05
35	P4	68.1	31.9	4.06
	P5	72.5	27.5	5.01

40 Note: The molar ratios as indicated with the symbol "*" are values calculated as moles of glucose against one mole of trehalose.

45 The results in Tables 3 and 4 strongly show that the saccharides P1 to P5 consist of one mole of trehalose and 1 to 5 moles of glucose. From the facts that glucoamylase specifically hydrolyzes the α -1,4 and α -1,6 linkages in maltooligosaccharides and that β -amylase hydrolyzes the α -1,4 linkage in maltooligosaccharides from their end terminals by maltose units, it is estimated that the saccharides P1 to P5 have a structure consisting of glucose or maltooligosaccharide having a degree of glucose polymerization of 2 to 5, both of which have a trehalose residue at their end terminals.

50 The total judgement of the above results identifies the saccharides P1 to P5 as α -glucosyl trehalose, α -maltosyl trehalose, α -maltotriosyl trehalose, α -maltotetraosyl trehalose and α -maltopentaosyl trehalose respectively, and this evidences that the enzymes have an activity of forming non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher.

Experiment 2-2Molecular weight

5 In accordance with the method reported by U. K. Laemmli in *Nature*, Vol.227, pp.680-685 (1970), the purified enzymes M-11 and Q36 in Experiment 1 were respectively electrophoresed on sodium dodecyl polyacrylamide gel electrophoresis to give a single protein band at a position corresponding to about 76,000-87,000 daltons. The marker proteins used in this experiment were myosin (MW=200,000 daltons), β -galactosidase (MW=116,250 daltons), phosphorylase B (MW=97,400 daltons), serum albumin (MW=66,200 daltons) and 10 ovalbumin (MW=45,000 daltons).

Experiment 2-3Isoelectric point

15 The purified enzymes M-11 and Q36 obtained in Experiment 1 gave an isoelectric point of about 3.6-4.6 on isoelectrophoresis respectively.

Experiment 2-4Optimum temperature

20 The optimum temperature of the purified enzymes M-11 and Q36 obtained in Experiment 1 was about 35-40°C as shown in FIG. 1 or 2 when incubated in usual manner in 50 mM phosphate buffer (pH 7.0) for 60 min.

Experiment 2-5Optimum pH

25 The optimum pH of the purified enzymes M-11 and Q36 obtained in Experiment 1 was about 6.4-7.2 as shown in FIG. 3 or 4 when experimented in usual manner by incubating them at 40°C for 60 min in 50 mM acetate buffer, phosphate buffer or sodium carbonate-sodium hydrogen carbonate buffer having different pHs.

Experiment 2-6Thermal stability

30 The purified enzymes M-11 and Q36 obtained in Experiment 1 were stable up to a temperature of about 35-40°C as shown in FIGs. 5 and 6 when experimented in usual manner by incubating them in 50 mM phosphate buffer (pH 7.0) for 60 min.

Experiment 2-7pH Stability

35 The purified enzymes M-11 and Q36 obtained in Experiment 1 were stable up to a pH of about 5.5-11.0 as shown in FIGs. 7 and 8 when experimented in usual manner by incubating them at 25°C for 16 hours in 50 mM acetate buffer, phosphate buffer or sodium carbonate-sodium hydrogen carbonate buffer having different pHs.

Experiment 2-8Amino acid sequence containing the N-terminal

40 The amino acid sequence containing the N-terminal of the purified enzyme M-11 obtained in Experiment 1 was analyzed on "MODEL 470 A", a gas-phase protein sequencer commercialized by Applied Biosystems, Inc., Foster City, USA, to reveal that enzyme M-11 has an amino acid sequence as shown in SEQ ID NO:12. The amino acid sequence containing the N-terminal of the purified enzyme Q36 was analyzed similarly

as in enzyme M-11 to reveal that it has an amino acid sequence as shown in SEQ ID NO:13.

Experiment 2-9

5 Partial amino acid sequence

An adequate amount of the purified enzyme M-11 obtained in Experiment 1-1 was weighed, dialyzed against 10 mM Tris-HCl buffer (pH 9.0) at 4°C for 18 hours, and admixed with 10 mM Tris-HCl buffer (pH 9.0) to give a concentration of about one mg/ml of the enzyme. About one ml of the resultant solution was placed in a container, admixed with 10 µg lysyl endopeptidase, and incubated at 30°C for 22 hours to partially hydrolyze the enzyme. The resultant hydrolysate was applied to "CAPCELL-PAK C18", a column for reverse-phase high-performance liquid chromatography commercialized by Shiseido Co., Ltd., Tokyo, Japan, which had been previously equilibrated with 0.1 v/v % trifluoroacetate containing 16 v/v % aqueous acetonitrile, followed by feeding to the column 0.1 v/v % trifluoroacetate at a flow rate of 0.9 ml/min while increasing the concentration of acetonitrile from 16 to 64 v/v % to separatory collect fractions containing a peptide fragment about 28 min or 40 min after the initiation of feeding (the peptide fragments were respectively named "peptide fragment A" and "peptide fragment B"). Fractions containing the peptide fragment A or B were separatory pooled, dried *in vacuo*, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Similarly as in Experiment 2-8, the peptide fragments A and B were analyzed and revealed to have an amino acid sequence as shown in SEQ ID NO:14 and an amino acid sequence as shown in SEQ ID NO:15.

Similarly as in enzyme M-11, enzyme Q36 obtained in Experiment 1-2 was partially hydrolyzed, and the resultant was fed to "μBONDAPAK C18", a column for reverse-phase high-performance liquid chromatography commercialized by Japan Millipore Ltd., Tokyo, Japan, followed by feeding to the column 0.1 v/v % trifluoroacetate containing aqueous acetonitrile ranging from a concentration of 24 v/v % to 44 v/v % at a flow rate of 0.9 ml/ml. Fractions containing a peptide fragment eluted about 22 min or about 40 min after the initiation of feeding (the fractions were respectively called "peptide fragment C" and "peptide fragment D" hereinafter) were respectively collected, pooled, dried *in vacuo*, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Analyses of the peptide fragments C and D conducted similarly as above revealed that they have amino acid sequences as shown in SEQ ID NOs:16 and 17, respectively.

No enzyme having these physicochemical properties has been known, and this concluded that it is a novel substance. Referring to *Rhizobium* sp. M-11, it is a microorganism which was isolated from a soil of Okayama-city, Okayama, Japan, deposited on December 24, 1992, in National Institute of Bioscience and Human-Technology Agency of Industrial Science and Technology, Tsukuba, Ibaraki, Japan, and accepted under the accession number of FERM BP-4130, and it has been maintained by the institute. *Arthrobacter* sp. Q36 is a microorganism which was isolated from a soil of Soja-city, Okayama, Japan, deposited on June 3, 1993, in the same institute, and accepted under the accession number of FERM BP-4316, and it has been maintained by the institute. Japanese Patent Application No.349,216/93 applied by the same applicant discloses the properties and features of the non-reducing saccharide-forming enzyme as well as the detailed bacteriological properties of these microorganisms.

The present inventors energetically screened a chromosomal DNA of *Rhizobium* sp. M-11 by using an oligonucleotide as a probe which had been chemically synthesized based on the partial amino acid sequence of enzyme M-11 as revealed in Experiment 2-9, and found a DNA fragment which consists of 2,316 base pairs having a base sequence as shown in the following SEQ ID NO:1 which initiates from the 5'-terminus. The decoding of the base sequence revealed that the enzyme consists of 772 amino acids as shown in SEQ ID NO:2.

Similarly as in enzyme M-11, a chromosomal DNA of enzyme Q36 was screened by using an oligonucleotide as a probe which had been chemically synthesized based on a partial amino acid sequence of enzyme Q36, and this yielded a DNA fragment having a base sequence consisting of 2,325 base pairs from the 5'-terminus as shown in SEQ ID NO:3. The base sequence was decoded to reveal that enzyme Q36 consists of 775 amino acids and has a partial amino acid sequence containing the N-terminal as shown in SEQ ID NO:4.

The sequential experimental steps used to reveal the base sequence and amino acid sequence as shown in SEQ ID NOs:1 to 4 are summarized as below:

- (1) The enzyme was isolated from a culture of a donor microorganism and highly purified. The purified enzyme was partially hydrolyzed with protease, and the resultant 2 different types of peptide fragments were isolated and determined their amino acid sequences;
- (2) Separately, a chromosomal DNA was isolated from a donor microorganism's cell, purified and partially digested by a restriction enzyme to obtain a DNA fragment consisting of about 3,000-7,000 base pairs. The DNA fragment was ligated by DNA ligase to a plasmid vector, which had been previously cut with a restriction enzyme, to obtain a recombinant DNA;

(3) The recombinant DNA was introduced into *Escherichia coli* to obtain transformants, and from which an objective transformant containing a DNA encoding the enzyme was selected by the colony hybridization method using as a probe an oligonucleotide which had been chemically synthesized based on the aforesaid partial amino acid sequence; and

5 (4) The recombinant DNA was obtained from the transformant and annealed with a primer, followed by allowing a DNA polymerase to act on the resultant to extend the primer, and determining the base sequence of the resultant complementary chain DNA by the dideoxy chain termination method. The comparison of an amino acid sequence estimable from the determined base sequence with the aforesaid amino acid sequence confirmed that the base sequence encodes the enzyme.

10 As is explained in the above, the enzyme, which forms non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher, is an enzyme which was found as a result of the present inventors' long-term research. The enzyme has distinct physicochemical properties from those of other conventional enzymes. The present invention is to produce the enzyme by applying recombinant DNA technology. The recombinant DNA, and its preparation and uses are explained in detail with reference to examples.

15 The recombinant enzyme as referred to in the invention means the whole enzymes which are preparable by recombinant DNA technology and capable of forming non-reducing saccharides having trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. Generally, the recombinant enzyme according to the present invention has a revealed amino acid sequence, 20 and, as an example, the amino acid sequence, which initiates from the N-terminal as shown in SEQ ID NO:2 or 4, and homologous ones to it can be mentioned. Variants having amino acid sequences homologous to the one as shown in SEQ ID NO:2 or 4 can be obtained by replacing one or more bases in SEQ ID NO:2 or 4 with other bases without substantially alternating the inherent action of the enzyme. Although even when used the same DNA and it also depends on hosts into which the DNA is introduced, ingredients and components of nutrient culture media for culturing transformants, and their cultivation temperature and pH, there may be produced modified enzymes which have amino acid sequences similar to that of SEQ ID NO:2 or 4 as well as having an enzymatic action of the enzyme encoded by the DNA but defecting one or more amino acids located nearness to the N-terminal of the amino acid sequence as shown in SEQ ID NO:2 or 4 and/or having one or 25 more amino acids newly added after the DNA expression to the N-terminal by the modification of intracellular enzymes of hosts. The recombinant enzyme can be obtained from cultures of transformants containing a specific DNA. Examples of such a transformant used in the invention can be prepared by introducing into hosts a DNA having either the base sequence which initiates from the N-terminal or a homologous base sequence to it or a complementary base sequence to them. Such a base sequence may be prepared by replacing one or more bases thereof without alternating the amino acid sequence encoded thereby by using degeneracy of 30 genetic code. Needless to say, one or more bases in the base sequence, which encodes the enzyme or their variants, can be readily replaced with other bases to allow the DNA to actually express the enzyme production in hosts.

35 The DNA usable in the present invention includes any one of those derived from natural resources and artificially synthesized ones as long as they have such an aforementioned base sequence. The natural resources for the DNA according to the present invention are, for example, microorganisms of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curtobacterium*, *Mycobacterium* and *Terrabacter*, i.e. *Rhizobium* sp. M-11 (FERM BP-4130), *Arthrobacter* sp. Q36 (FERM BP-4316), *Brevibacterium helovolum* (ATCC 11822), *Flavobacterium aquatile* (IFO 3772), *Micrococcus luteus* (IFO 3064), *Micrococcus roseus* (ATCC 186), *Curtobacterium citreum* (IFO 15231), *Mycobacterium smegmatis* (ATCC 19420) and *Terrabacter tumescens* (IFO 12960) from which genes containing the present DNA can be obtained. The aforementioned microorganisms can be inoculated in nutrient culture media and cultured for about 1-3 days under aerobic conditions, and the resultant cells were collected from the cultures and subjected to ultrasonication or treated with a cell-wall lysis enzyme such as lysozyme or β -glucanase to extract genes containing the present DNA. In this case, a proteolytic enzyme such as protease can be used along with the cell-wall lysis enzyme, and, in the 40 case of treating the cells with an ultrasonic disintegrator; they may be treated in the presence of a surfactant such as sodium dodecyl sulfate (SDS) or may be treated with freezing and thawing. The objective DNA is obtainable by treating the resultant with phenol extraction, alcohol sedimentation, centrifugation, protease treatment and/or ribonuclease treatment used in general in this field. To artificially synthesize the present DNA, it can be chemically synthesized by using the base sequence as shown in SEQ ID NO:1 or 3, or can be obtained in a plasmid form by inserting a DNA which encodes the amino acid sequence as shown in SEQ ID NO:2 or 4 into an appropriate self-replicable vector to obtain a recombinant DNA, introducing the recombinant DNA into an appropriate host to obtain a transformant, culturing the transformant, separating the proliferated cells from the resultant culture, and collecting plasmids containing the DNA from the cells.

Such a recombinant DNA is generally introduced into hosts in a recombinant DNA form. Generally, the recombinant DNA contains the aforesaid DNA and a self-replicable vector, and it can be prepared with a relative easiness by recombinant DNA technology in general when the material DNA is in hand. Examples of such a vector are plasmid vectors such as pBR322, pUC18, Bluescript II SK(+), pUB110, pTZ4, pC194, pHV14, TRP7, TEp7, pBS7, etc.; and phage vectors such as λgt·λC, λgt·λB, p11, φ1, φ105, etc. Among these plasmid- and phage-vectors, pBR322, pUC18, Bluescript II SK(+), λgt·λC and λgt·λB are satisfactorily used when the present DNA needs to be expressed in *Escherichia coli*, while pUB110, pTZ4, pC194, p11, φ1 and φ105 are satisfactorily used to express the DNA in microorganisms of the genus *Bacillus*. The plasmid vectors pHV14, TRP7, TEp7 and pBS7 are advantageously used when the recombinant DNA is allowed to grow in 2 or more hosts.

The methods used to insert the present DNA into such a vector in the invention may be conventional ones in general in this field. A gene containing the present DNA and a self-replicable vector are first digested by a restriction enzyme and/or ultrasonic disintegrator, then the resultant DNA fragments and vector fragments are ligated. To digest DNAs and vectors, restriction enzymes which specifically act on nucleotides, particularly, type II restriction enzymes, more particularly *Sau* 3AI, *Eco* RI, *Hind* III, *Bam* HI, *Sal* I, *Xba* I, *Sac* I, *Pst* I, etc., facilitate the ligation of the DNA fragments and vector fragments. To ligate the DNA fragments with vector fragments, they are annealed if necessary, then subjected to the action of a DNA ligase in vivo or in vitro. The recombinant DNA thus obtained is replicable without substantial limitation by introducing it into appropriate hosts, and culturing the resultant transformants.

The recombinant DNA thus obtained can be introduced into appropriate host microorganisms including *Escherichia coli* and those of the genus *Bacillus* as well as actinomycetes and yeasts. In the case of using *Escherichia coli* as a host, the DNA can be introduced thereinto by culturing the host in the presence of the recombinant DNA and calcium ion, while in the case of using a microorganism of the genus *Bacillus* as a host the competent cell method and the colony hybridization method can be employed. Desired transformants can be cloned by the colony hybridization method or by culturing a variety of transformants in nutrient culture media containing reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher, and selecting the objective transformants which form non-reducing amyloseous saccharides having trehalose structure as an end unit from the reducing amyloseous saccharides.

The transformants thus obtained extracellularly produce the objective enzyme when cultured in nutrient culture media. Generally, liquid culture media in general supplemented with carbon sources, nitrogen sources and minerals, and, if necessary, further supplemented with small amounts of amino acids and vitamins can be used in the invention. Examples of the carbon sources are saccharides such as starch, starch hydrolysate, glucose, fructose and sucrose. Examples of the nitrogen sources are organic- and inorganic-substances containing nitrogen such as ammonia, ammonium salts, urea, nitrate, peptone, yeast extract, defatted soy bean, corn steep liquor, and beef extract. Cultures containing the objective enzyme can be prepared by inoculating the transformants into nutrient culture media, and incubating them at a temperature of 25-65°C and a pH of 2-8 for about 1-6 days under aerobic conditions by aeration and agitation. Such a culture can be used intact as an enzyme agent, and, usually, it may be disrupted prior to use with ultrasonic disintegrator and/or cell-wall lysis enzymes, followed by separating the enzyme from the intact cells and cell debris by filtration and/or centrifugation and purifying the enzyme. The methods to purify the enzyme include conventional ones in general. From cultures intact cells and cell debris are eliminated and subjected to one or more methods such as concentration, salting out, dialysis, preparatory sedimentation, gel filtration chromatography, ionexchange chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectric point electrophoresis.

As is described above, the recombinant enzyme according to the present invention has a specific feature of forming non-reducing saccharides having trehalose structure as an end unit from reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher. The formed non-reducing saccharides have a satisfactorily mild and high-quality sweetness as well as an adequate viscosity and moisture-retaining ability, and, as a great advantageous feature, they can sweeten food products without fear of causing coloration and deterioration because they do not have a reducing residue within their molecule. By using these features a variety of amyloseous saccharides, which have been put aside because of their reducibilities, can be converted into saccharides having a satisfactory handleability and usefulness but having substantially no or extremely-reduced reducibility.

Now explaining the conversion method in more detail, reducing starch hydrolysates, which are obtainable by partially hydrolyzing amyloseous saccharides such as starch, amylopectin and amylose by acids and/or amylases, can be usually used as the substrate for the present recombinant enzyme. Such a starch hydrolysate can be obtained by conventional methods in general used in the art, and examples thereof include one or more maltooligosaccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltopentaose, maltohexaose and maltoheptaose. As described in "Handbook of Amylases and Re-

Iated Enzymes", 1st edition, edited by Th Amylase Research Society of Japan, published by Pergamon Press plc, Oxford, England (1988), α -amylase, maltotetraose-forming amylase, maltpentaose-forming amylase and maltohexaose-forming amylase are especially useful to prepare the reducing amyloseous saccharides used in the invention, and, the use of any one of these amylases readily yields amyloseous saccharide mixtures rich in reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher in a considerably-high yield. If necessary, the combination use of the amylases and starch debranching enzymes such as pullulanase and isoamylase can increase the yield of the reducing amyloseous saccharides used as the substrate for the present recombinant enzyme.

In the conversion method according to the present invention, the present recombinant enzyme is allowed to coexist in an aqueous solution containing one or more of the aforesaid reducing amyloseous saccharides as a substrate, and allowing the solution to enzymatically react at a prescribed temperature and pH until a desired amount of the objective reducing amyloseous saccharides is formed. Although the enzymatic reaction proceeds even below a concentration of 0.1 w/v % of a substrate, a higher concentration of 2 w/v %, preferably, 5-50 w/v % of a substrate can be satisfactorily used to apply the present conversion method to an industrial-scale production. The temperature and pH used in the enzymatic reaction are set within the ranges of which do not inactivate the recombinant enzyme and allow the recombinant enzyme to effectively act on substrates, i.e. a temperature up to about 55°C, preferably, a temperature in the range of about 40-55°C, and a pH of 5-10, preferably, a pH in the range of about 6-8. The amount and reaction time of the present recombinant enzyme are chosen dependently on the enzymatic reaction condition. The enzymatic reaction relatively-highly reduces the reducing power of reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher, and, in the case of maltpentaose, the reducing powder is lowered to about 7% against the original level.

The reaction mixtures obtained by the present conversion reaction can be used intact, and, usually, they are purified prior to use: Insoluble substances are eliminated from the reaction mixtures by filtration and centrifugation, and the resultant solutions are decolorized with an activated charcoal, desalted and purified on ion exchangers, and concentrated into syrupy products. Dependently on their use, the syrupy products are dried *in vacuo* and spray-dried into solid products. In order to obtain products which substantially consist of non-reducing saccharides, the aforesaid syrupy products are subjected to one or more methods such as chromatography using an ion exchanger, activated charcoal and silica gel for saccharide separation, separatory sedimentation using alcohol and/or acetone, membrane filtration, fermentation by yeasts, and removal and decomposition of reducing saccharides by alkalis. The methods to treat a large amount of reaction mixture are, for example, fixed bed- or pseudomoving bed-ion exchange column chromatography as disclosed in Japanese Patent Laid-Open Nos.23,799/83 and 72,598/83, and such a method produces non-reducing saccharide-rich products in an industrial scale and in a considerably-high yield.

The reducing saccharides thus obtained have a wide applicability to a variety of products which are apt to be readily damaged by the reducibility of saccharide sweeteners: For example, they can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. Since the non-reducing saccharides approximately qualitatively form trehalose when received an enzymatic action of a trehalose-releasing enzyme as disclosed in Japanese Patent Application No.340,343/93, they can be used as an intermediate for the production of trehalose which could not have been readily prepared.

The following examples explain the present invention in more detail, and the recombinant DNA technologies or techniques employed therein are in themselves conventional ones used in the art, for example, those described by J. Sumbruck et al. in "*Molecular Cloning A Laboratory Manual*", 2nd edition, published by Cold Spring Harbor Laboratory Press, USA (1989).

Example 1

Preparation of recombinant DNA containing DNA derived from enzyme M-11, and transformant

Example 1-1

Preparation of chromosomal DNA

A seed culture of *Rhizobium* sp. M-11 was inoculated into bacto nutrient broth medium (pH 7.0), and cultured at 27°C for 24 hours with a rotary shaker. The cells were separated from the resultant culture by centrifugation, suspended in TES buffer (pH 8.0), admixed with 0.05 w/v % lysozyme, and incubated at 37°C for 30 min. The resultant was freezed at -80°C for one hour, admixed with TSS buffer (pH 9.0), heated to 60°C, and admixed with a mixture solution of TES buffer and phenol, and the resultant solution was chilled with ice, fol-

lowed by centrifugally collecting the precipitated crude chromosomal DNA. To the supernatant was added 2 fold volumes of cold ethanol, and the precipitated crude chromosomal DNA was collected, suspended in SSC buffer (pH 7.1), admixed with 7.5 µg ribonuclease and 125 µg protease, and incubated at 37°C for one hour. Thereafter, a mixtur solution of chloroform and isoamyl alcohol was added to the reaction mixture to extract the objective chromosomal DNA, and admixed with cold ethanol, followed by collecting the formed sediment containing the chromosomal DNA. The purified chromosomal DNA thus obtained was dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the solution was freezed at -80°C.

Example 1-2

10

Preparation of recombinant DNA pBMT7 and transformant BMT7

About one ml of the purified chromosomal DNA obtained in Example 1-1 was placed in a container, admixed with about 35 units of *Sau* 3AI, a restriction enzyme, and enzymatically reacted at 37°C for about 20 min to partially digest the chromosomal DNA, followed by recovering a DNA fragment consisting of about 3,000-7,000 base pairs by sucrose density-gradient ultracentrifugation. One µg of Bluescript II SK(+), a plasmid vector, was provided, subjected to the action of *Bam* HI, a restriction enzyme, to completely digest the plasmid vector, admixed with 10 µg of the DNA fragment and 2 units of T4 DNA ligase, and allowed to stand at 4°C overnight to ligate the DNA fragment to the vector fragment. To the resultant recombinant DNA was added 30 µl of "Epicurian *Coli*® XLI-Blue", competent cell commercialized by Toyobo Co., Ltd., Tokyo, Japan, allowed to stand under ice-chilled conditions for 30 min, heated to 42°C admixed with SOC broth, incubated at 37°C for one hour to introduce the recombinant DNA into *Escherichia coli*.

The resultant transformant was inoculated into agar plate (pH 7.0) containing 50 µg/ml of 5-bromo-4-chloro-3-indolyl-β-galactoside, and cultured at 37°C for 18 hours, followed by placing a nylon film on the agar plate to fix thereon about 4,400 colonies formed on the agar plate. Based on the amino acid sequence of Pro-Glu-Trp-Glu-Lys located at positions from 17 to 21 in the amino acid sequence of the peptide fragment A as revealed in Experiment 2-9, the base sequence of probe 1 as shown in SEQ ID NO:5 was chemically synthesized, labelled with ³²P, and hybridized with the colonies of transformants fixed on the nylon film, followed by selecting 9 transformants which exhibited a strong hybridization.

The objective recombinant DNA was selected in usual manner from the 9 transformants, and, in accordance with the method described by E. M. Southern in *Journal of Molecular Biology*, Vol.98, pp.503-517 (1975), hybridized with probe 2 having the base sequence as shown in SEQ ID NO:6 which had been chemically synthesized based on the amino acid sequence of Thr-Glu-Phe-Trp-Asp located at positions from 16 to 20 in the amino acid sequence of the peptide fragment B as revealed in Experiment 2-9, followed by selecting a recombinant DNA which strongly hybridized with probe 2. The recombinant DNA and transformant thus selected were respectively named pBMT7 and BMT7.

The transformant BMT7 obtained in the above was inoculated into L-broth (pH 7.0) containing 100 µg/ml ampicillin, and cultured at 37°C for 24 hours with a rotary shaker. After completion of the culture, the cells were collected from the culture by centrifugation, and treated with the alkaline method in general to extracellularly extract a recombinant DNA. The resultant was in usual manner purified and analyzed to find that the recombinant DNA pBMT7 consists of about 9,300 base pairs and has a structure expressed by the restriction map as shown in FIG. 9. It was revealed that as shown in FIG. 9 the DNA consisting of 2,316 base pairs encoding enzyme M-11 is located in the downstream near to the digested site by *Pst* I, a restriction enzyme.

45 Example 1-3

Production of enzyme by transformant

A liquid medium consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate was adjusted to pH 7.0, admixed with 50 µg/ml ampicillin, autoclaved at 120°C for 20 min, cooled and inoculated with a seed culture of transformant BMT7 obtained in Example 1-2, followed by culturing the transformant at 37°C for 24 hours with a rotary shaker. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to find that one L of the culture yielded about 3,000 units of the enzyme.

As a control, a seed culture of *Escherichia coli* XLI-Blue or *Rhizobium* sp. M-11 was inoculated into a fresh preparation of the same liquid culture medium but free of ampicillin, and, in the case of the culture of *Rhizobium* sp. M-11, it was cultured and treated similarly as above except that the culturing temperatur was set to 30°C.

Assaying the resultant activity, one L culture of *Rhizobium* sp. M-11 yielded about 1,500 units of the enzyme, and the yield was significantly lower than that of transformant BMT7. *Escherichia coli* XLI-Blue used as a host did not form the enzyme.

Thereafter, the enzyme produced by the transformant BMT7 purified similarly as in Experiment 1-1, and examined on the properties and characteristics. As a result, it was revealed that it has substantially the same physicochemical properties as that of Experiment 2 showing a molecular weight of about 76,000-87,000 daltons on SDS-PAGE and an isoelectric point of about 3.6-4.6 on isoelectrophoresis. The results indicate that the present enzyme can be prepared by recombinant DNA technology, and the yield is significantly increased thereby.

10

Example 2

Preparation of complementary DNA derived from enzyme M-11 and determination of its base sequence and amino acid sequence

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Two µg of the recombinant DNA pBMT7 obtained by the method in Example 1-2 was weighed, admixed with 2 M aqueous sodium hydroxide solution to effect degeneration, and admixed with an adequate amount of cold ethanol, followed by collecting the resultant sediment containing a template DNA and drying the sediment in vacuo. To the template DNA were added 50 pmole/ml of a chemically synthesized primer 1 having the base sequence as shown in SEQ ID NO:7, and 10 µl of 40 mM Tris-HCl buffer (pH 7.5) containing 20 mM magnesium chloride and 50 mM sodium chloride, and incubated at 65°C for 2 min to effect annealing, and the mixture was admixed with 2 µl of an aqueous solution containing dATP, dGTP and dTTP in respective amounts of 7.5 µM, 0.5 µl of [α -³²P]dCTP (2 mCi/ml), one µl of 0.1 M dithiothreitol, and 2 µl of 1.5 units/ml T7 DNA polymerase, followed by incubating the resultant mixture at 25°C for 5 min to extend the primer 1 from the 5'-terminus to the 3'-terminus. Thus, a complementary chain DNA was formed.

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The reaction product containing the complementary chain DNA was divided into quarters, to each of which 2.5 µl of 50 mM aqueous sodium chloride solution containing 80 µM dNTP and 8 µM ddATP, ddCTP, ddGTP or ddTTP was added, and the resultant mixture was incubated at 37°C for 5 min, followed by suspending the reaction by the addition of 4 µl of 95 v/v % aqueous formamide solution containing 20 mM EDTA, 0.05 w/v % bromophenol blue and 0.05 w/v % xylene cyanol. The reaction mixture was placed in a container, heated in a boiling-water bath for 3 min, placed on a gel containing 6 w/v % polyacrylamide, and electrophoresed by energizing the gel with a constant voltage of about 2,000 volts to separate DNA fragments, followed by fixing the gel in usual manner, drying and subjecting the resultant gel to autoradiography.

25

Analyses of the DNA fragments separated on the radiogram revealed that the complementary chain DNA contains the base sequence consisting of 2,936 base pairs as shown in SEQ ID NO:10. An amino acid sequence estimable from the base sequence was as shown in SEQ ID NO:10, and it was compared with the amino acid sequence containing the N-terminal and the partial amino acid sequence of enzyme M-11 as shown in SEQ ID NO:12, 14 or 15, and found that the amino acid sequence containing the N-terminal of SEQ ID NO:12 corresponded to the amino acid sequence at positions from 1 to 20 of SEQ ID NO:10, and the partial amino acid sequence of SEQ ID NO:14 or 15 corresponded to the amino acid sequence at positions from 486 to 506 or at positions from 606 to 626 of SEQ ID NO:10. The results indicate that the enzyme produced from *Rhizobium* sp. M-11 has the amino acid sequence of SEQ ID NO:2, and the enzyme derived from the microorganism is encoded by the DNA having the base sequence as shown in SEQ ID NO:1.

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Example 3

Preparation of recombinant DNA containing DNA derived from *Arthrobacter* sp. Q36 and transformant

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Example 3-1

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Preparation of chromosomal DNA

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Similarly as in Example 1-1, a chromosomal DNA was isolated from *Arthrobacter* sp. Q36, purified and dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the resultant solution was freezed at -80°C.

Example 3-2Preparation of recombinant DNA pBQT13 and transformant BQT13

5 The purified chromosomal DNA obtained in Example 3-1 was partially digested similarly as in Example 1-2, followed by recovering a DNA fragment consisting of about 3,000-6,000 base pairs by sucrose density gradient ultracentrifugation. The DNA fragment was ligated to a lysate of Bluescript II SK(+) which had been treated with *Bam* HI similarly as in Example 1-2, and the resultant recombinant DNA was introduced into *Escherichia coli* XLI-Blue. The transformants thus obtained were cultured similarly as in Example 1-2 in an agar plate containing 5-bromo-4-chloro-3-indolyl- β -D-galactoside, and the resultant about 4,500 colonies were fixed on a nylon film, while probe 3 having the base sequence as shown in SEQ ID NO:8 was chemically synthesized based on the amino acid sequence as expressed by Phe-Asp-Val-Asp-Trp-Asp, which are located at positions from 11 to 16 in the amino acid sequence of the peptide fragment D as shown in SEQ ID NO:17, labelled with 32 P, and hybridized with transformant colonies which had been fixed on the nylon film, followed by selecting 10 15 8 transformants which strongly hybridized with probe 3.

Similarly as in Example 1-2, the objective recombinant DNA was selected from the 8 transformants, and hybridized with probe 4 having the base sequence as shown in SEQ ID NO:9 which had been chemically synthesized based on the amino acid sequence located at positions from 16 to 20, i.e. Thr-Glu-Phe-Trp-Asp, in SEQ ID NO:16, followed by selecting a recombinant DNA which strongly hybridized with probe 4. The recombinant DNA and transformant thus selected were respectively named pBQT13 and BQT13.

The transformant BQT13 was inoculated into L-broth containing ampicillin, and cultured similarly as in Example 3-2, and the proliferated cells were collected from the resultant culture, and from which a recombinant DNA was extracted, purified and analyzed to reveal that the recombinant pBQT13 consists of about 7,200 base pairs and has a structure expressed by the restriction map as shown in FIG. 10. As shown in FIG. 3, it was 20 25 reveal that the DNA, which consists of 2,325 base pairs and encodes the DNA of enzyme Q36, is located in the downstream near the cleavage site of *Xmn* I.

Example 3-3Production of enzyme by transformant BQT13

A liquid culture medium consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate was adjusted to pH 7.0, admixed with 50 μ g/ml ampicillin, autoclaved at 120°C for 20 min, cooled and inoculated with a seed culture of the transformant BQT13 obtained in Example 3-2, followed by culturing the transformant at 37°C for 24 hours by a rotary shaker. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to find that one L of the culture yielded about 2,450 units of the enzyme.

As a control, *Escherichia coli* XLI-Blue or *Arthrobacter* sp. Q36 was inoculated in a fresh preparation of 40 the same liquid culture medium but free of ampicillin, and cultured and treated similarly as above except that the culturing temperature was set to 30°C. The assay of the activity of the resultants showed that one L of the culture of *Arthrobacter* sp. Q36 yielded about 1,200 units of the enzyme, and the level of which was significantly lower than that of the transformant BQT13. *Escherichia coli* XLI-Blue used as a host did not form the enzyme.

Thereafter, the enzyme produced by the transformant BMT7 was purified similarly as in Experiment 1-1, and examined on the properties and characteristics. As a result, it was revealed that it has substantially the same physicochemical properties as shown in Experiment 2 of a molecular weight of about 76,000-87,000 daltons on SDS-PAGE and an isoelectric point of about 3.6-4.6 on Isoelectrophoresis.

The results indicate that the enzyme can be prepared by recombinant DNA technology, and the yield might 50 be significantly increased thereby.

Example 4Preparation of complementary chain DNA derived from *Arthrobacter* sp. Q36, and determination of its base sequence and amino acid sequence

The recombinant DNA pBQT13 obtained in Example 3-2 was similarly treated as in Example 2 to form a template DNA which was then annealed together with the primer 1, followed by allowing T7 DNA polymerase

to act on the resultant to extend the primer 1 from the 5'-terminus to 3'-terminus to obtain a complementary chain DNA. Similarly as in Example 2, the complementary chain DNA was subjected to the dideoxy chain terminator method to analyze DNA fragments isolated on a radiogram. The result revealed that the complementary chain DNA contained a base sequence consisting of 3,073 base pairs and an amino acid sequence estimable from the base sequence were as shown in SEQ ID NO:11. The amino acid sequence was compared with respect to the amino acid sequence containing the N-terminal and the partial amino acid sequence of SEQ ID NO:13, 16 or 17, and found that the amino acid sequence containing the N-terminal of SEQ ID NO:13 corresponded to that located at positions from 1 to 20 in SEQ ID NO:11, and the partial amino acid sequence of SEQ ID NO:16 and 17 corresponded to the amino acid sequence located at positions from 606 to 625 or from 110 to 129 in SEQ ID NO:11. The results indicate that enzyme Q36 has the amino acid sequence of SEQ ID NO:4, and it is encoded by the DNA having the base sequence as shown in SEQ ID NO:3.

Example 5

Preparation of recombinant enzyme

In 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid culture medium (pH 7.0) consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate, and to each flask was added 50 µg/ml ampicillin and autoclaved at 120°C for 20 min. Thereafter, the flasks were cooled and inoculated with the transformant BMT7 obtained in Example 1-2, followed by culturing the transformant at 27°C for 24 hours by a rotary shaker. Apart from this, 18 L of a fresh preparation of the same liquid culture medium was placed in an Erlenmeyer flask, admixed with 50 µg/ml ampicillin, sterilized at 120°C for 20 min, cooled and inoculated with one v/v % of the seed culture obtained in the above, followed by the culture at 37°C for 24 hours under aeration and agitation conditions. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to show that one L of the culture yielded about 3,000 units of the enzyme. The supernatant was purified by the method in Experiment 1-1 to obtain an about 50 ml aqueous solution containing about 135 units/ml of a recombinant enzyme having a specific activity of about 200 units/mg protein.

Example 6

Preparation of recombinant enzyme

Recombinant BQT13 obtained by the method in Example 3-2 was cultured similarly as in Example 5, and the resultant culture was treated with an ultrasonic integrator to disrupt cells. The resultant suspension was centrifuged to remove insoluble substances, and the resultant supernatant was assayed for the enzyme activity to reveal an enzyme production of about 2,450 units per L of the culture. The supernatant was purified by the method in Experiment 1-1 to obtain an about 45 ml aqueous solution containing about 120 units/ml of a recombinant enzyme having a specific activity of about 200 units/mg protein.

Example 7

Conversion of starch hydrolysate by recombinant enzyme

A potato starch was suspended in water to give a 6 w/w % suspension which was then autoclaved at 120°C for 10 min to gelatinize the starch. The gelatinized starch was rapidly cooled to 50°C, adjusted to a pH of about 4.5, admixed with 2,500 units/g starch, d.s.b., of an isoamylase specimen commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted at 50°C for 20 hours. The reaction mixture was adjusted to pH 6.0, autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, admixed with 150 units/g starch, d.s.b., of "TERMAMYL 60L", an α-amylase specimen commercialized by Novo Nordisk BioIndustri A/S, Copenhagen, Denmark, and enzymatically reacted at 45°C for 24 hours to obtain a reaction mixture containing reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The reaction mixture was autoclaved at 120°C for 20 min to inactivate the remaining enzyme, rapidly cooled to 45°C, admixed with one unit/g starch, d.s.b., of the recombinant enzyme obtained in Example 5, and enzymatically reacted at 45°C for 96 hours. The resultant reaction mixture was heated at 96°C for 10 min to inactivate the remaining enzyme, cooled and filtered, and the resultant filtrate was in usual manner decolorized with an activated charcoal, de-

salted and purified by an ion exchanger and concentrated to obtain an about 70 w/w % syrup, d.s.b., in a yield of about 91%, d.s.b.

Analysis of the syrup conducted by the method of Experiment 2-1 revealed that it had a DE (dextrose equivalent) of 18.7 and contained as a main component, on a dry solid basis, 8.4 w/w % α -glucosyl trehalose, 5.6 w/w % α -maltosyl trehalose, 37.9 w/w % α -maltotrioseyl trehalose, and that the greater part of the aforesaid reducing saccharides were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 8

15 Conversion of starch hydrolysate by recombinant enzyme

Potato starch was suspended in water to give a concentration of 33 w/w %, d.s.b., and the suspension was admixed with 0.1 w/w % calcium carbonate, d.s.b. The resultant suspension was admixed with 0.2 w/w % per g starch, d.s.b., of "TERMAMYL 60L", an α -amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 95°C for 15 min. The reaction mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled, admixed with 5 units/g starch, d.s.b., of a maltotetraose-forming amylase derived from *Pseudomonas stutzeri* as disclosed in Japanese Patent Laid-Open No.240,784/88, and enzymatically reacted at 55°C for 6 hours. Thereafter, the resultant reaction mixture was admixed with 30 units/g starch, d.s.b., of " α -amylase 2A", an α -amylase specimen commercialized by Ueda Chemical Co., Ltd., Osaka, Japan, and enzymatically reacted at 65°C for 4 hours to form about 50 w/w %, d.s.b., of reducing amyloseous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The resultant mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amyloseous saccharide, d.s.b., of the recombinant enzyme obtained in Example 5, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, decolorized in usual manner with an activated charcoal, desalts and purified with an ion exchanger, and concentrated to obtain a syrupy product with a concentration of about 70 w/w %, d.s.b., in a yield of about 90% against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 10.5 and contained as a main component 3.8 w/w % α -glucosyl trehalose, 43.8 w/w % α -maltosyl trehalose, and 1.2 w/w % α -maltotrioseyl trehalose, d.s.b., and that most of the reducing amyloseous saccharides contained therein were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

Example 9

45 Conversion of maltopentaose by recombinant enzyme

A high-purity maltopentaose produced by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, was dissolved in water to give a concentration of 20 w/w %, d.s.b., and the solution was adjusted to pH 6.5, admixed with one unit/g maltopentaose, d.s.b., of a recombinant enzyme obtained by the method in Example 5, and enzymatically reacted at 45°C for 48 hours. The reaction mixture was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, concentrated and analyzed by the method in Experiment 2-1 to find that about 92 w/w %, d.s.b., of the material maltopentaose was converted into α -maltotrioseyl trehalose.

Four jacketed-stainless steel columns, having a diameter of 5.4 cm and a length of 5 m each, were packed to homogeneity with "XT-1016 (Na⁺-form)", a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, and cascaded in series to give a total column length of 20 m. The reaction mixture obtained in the above was fed to the columns at a rate of about 5 v/v % against the resin at an inner column temperature of 55°C, and the columns were fed with 55°C hot water at an SV (space velocity) of 0.13 to elute saccharide components. Based on the saccharide composition analysis of the eluate,

fractions rich in non-reducing saccharides were collected, pooled, concentrated, dried *in vacuo* and pulverized to obtain a solid product in a yield of about 55%, d.s.b.

Analysis of the solid product by the method in Experiment 2-1 revealed that it had a DE less than about 0.2 and contained 99.0 w/w % α -maltotriosyl trehalose, d.s.b. The product, having a relatively-low hygroscopicity, a significantly-low reducibility as well as a slight sweetness, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

10 Example 10

Conversion of starch hydrolysate by recombinant enzyme

"PINE-DEX #4", a starch hydrolysate produced by Matsutani Chemical Ind., Co., Ltd., Kyoto, Japan, was dissolved in water to give a concentration of 40 w/w %, d.s.b., and the solution was heated to 45°C, adjusted to pH 6.5, admixed with one unit/g starch hydrolysate, d.s.b., of a recombinant enzyme obtained by the method in Example 5, and enzymatically reacted at for 96 hours to obtain a reaction mixture containing non-reducing saccharides having trehalose structure as an end unit. Thereafter, the reaction mixture was heated at 100°C for 10 min to inactivate the remaining enzyme, concentrated up to a 20 w/w % solution, d.s.b., cooled to 55°C, adjusted to pH 4.5, admixed with 10 units/g saccharide, d.s.b., of "GLUCOZYME", a glucoamylase specimen commercialized by Nagase Biochemicals, Ltd., Kyoto, Japan, and enzymatically reacted for 40 hours. The reaction mixture was heated at 100°C for 10 min to inactivate the remaining enzyme, cooled, decolored in usual manner with an activated charcoal, desalts and purified with an ion exchanger, and concentrated to obtain an about 60 w/w % syrupy product containing about 29.7 w/w % trehalose, d.s.b.

Similarly as in Example 9 except for using "CG6000 (Na⁺-form), the syrupy product was fractionated, followed by collecting fractions containing about 90 w/w % trehalose, d.s.b. The fractions were pooled, concentrated into an about 75 w/w % solution which was then transferred to a crystallizer, admixed with about 2 w/w % trehalose hydrate as a seed crystal against saccharides, d.s.b., and crystallized under gentle stirring conditions to obtain a massecuite with a crystallinity of about 45%. The massecuite was sprayed downward from a nozzle, equipped at the upper part of a spraying tower at a pressure of about 150 kg/cm² while about 85°C hot air was flowing downward from the upper part of the tower to accumulate a crystalline powder on a belt conveyer provided on the basement of the tower, followed by gradually transferring it out of the tower. Thereafter, the powder was transferred to an aging tower and aged for 10 hours to complete the crystallization and drying while an about 40°C hot air was blowing to the contents.

The product, having a substantial non-hygroscopicity and a mild and high-quality sweetness, can be satisfactorily used in food products, cosmetics, pharmaceuticals and feeds as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

Example 11

Conversion of starch hydrolysate by recombinant enzyme

Tapioca starch was suspended in water to give a concentration of 34 w/w % and admixed with 0.1 w/w % calcium carbonate. To the suspension was added 0.2 w/w % per g starch, d.s.b., of "TERMAMYL 60L", an α -amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 95°C for 15 min to liquefy the starch. The liquefied product was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 55°C, adjusted to pH 5.2, admixed with 10 units/g starch, d.s.b., of " α -amylase 2A", an α -amylase specimen commercialized by Ueda Chemical Co., Ltd., Osaka, Japan, and 500 units of an isoamylase specimen commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted at 55°C for 20 hours to form a mixture with a DE of about 29, containing about 60 w/w %, d.s.b., of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose, maltpentaose and maltohexaose. The mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of a recombinant enzyme obtained by the method in Example 6, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled, filtered, decolored in usual manner with an activated charcoal, desalts and purified with an ion exchanger, and concentrated to obtain a syrupy product with a concentration of about 70 w/w %, d.s.b., in a yield of about 90% against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 15.8 and contained as a main component 5.8 w/w % α -glucosyl trehalose, 8.5 w/w % α -maltosyl trehalose, 13.1 w/w % α -maltotriosyl trehalose, 18.9 w/w % α -maltotetraosyl trehalose and 3.6 w/w % α -maltopentaosyl trehalose, d.s.b., and that most of the reducing amylaceous saccharides contained therein were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

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Example 12

Conversion of starch hydrolysate by recombinant enzyme

Similarly as in Example 8, a liquefied potato starch was successively subjected to the action of maltotetraose-forming amylase and α -amylase to form a mixture containing about 50 w/w %, d.s.b., of reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher such as maltotriose, maltotetraose and maltopentaose. The reaction mixture was autoclaved at 120°C for 10 min to inactivate the remaining enzyme, rapidly cooled to 45°C, adjusted to pH 6.5, admixed with 2 units/g amylaceous saccharide, d.s.b., of a recombinant enzyme obtained by the method in Example 6, and enzymatically reacted at 45°C for 64 hours. The reaction mixture thus obtained was heated at 95°C for 10 min to inactivate the remaining enzyme, cooled and filtered, and the filtrate was decolored in usual manner with an activated charcoal, desalts and purified with an ion exchanger, and concentrated to obtain an about 70 w/w % syrupy product in a yield of about 90 w/w % against the material starch, d.s.b.

Analysis of the syrupy product by the method in Experiment 2-1 revealed that it had a DE of 10.3 and contained as a main component 3.6 w/w % α -glucosyl trehalose, 44.0 w/w % α -maltosyl trehalose and 1.0 w/w % α -maltotriosyl trehalose, d.s.b., and that most of the reducing amylaceous saccharides contained in the syrupy product were converted into their corresponding non-reducing saccharides. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant. The product contains non-reducing saccharides in a relatively-high content, so it can be also used as an intermediate for preparing trehalose.

As is described above, the present invention is based on the finding of a novel enzyme which forms non-reducing saccharides having trehalose structure as an end unit from reducing saccharides having a degree of glucose polymerization of 3 or higher. The present invention is to explore a way to produce such enzyme by recombinant DNA technology in a relatively-large scale and in a considerably-high yield. The conversion method using the present recombinant enzyme effectively converts reducing amylaceous saccharides into their corresponding non-reducing saccharides which have a mild and high-quality sweetness and an adequate viscosity and moisture-retaining ability, do not have a reducing residue within the molecules, and sweeten food products without fear of causing an unsatisfactory coloration and deterioration. In addition, the present recombinant enzyme is the one with a revealed total amino acid sequence, and because of this it can be used for the preparation of trehalose and non-reducing saccharides having trehalose structure as an end unit which are premised on being used in food products without fear of causing side effects.

Thus, the present invention is a significant invention which exerts the aforesaid outstanding action and effect as well as giving a great contribution to the field.

While there has been described what is at present considered to be the preferred embodiments of the invention, it will be understood the various modifications may be made therein, and it is intended to cover in the appended claims all such modifications as fall within the true spirits and scope of the invention.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
KENKYUJO

(ii) TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA
AND ENZYME, TRANSFORMANT, AND THEIR
PREPARATIONS AND USES

(iii) NUMBER OF SEQUENCES: 17

(iv) ADDRESS:

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KAGAKU KENKYUJO
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(D) STATE: JAPAN
(F) POSTAL CODE (ZIP): 700

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS

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(B3) FILING DATE: April 6, 1994
(A4) APPLICATION NUMBER: JP 90728/1994
(B4) FILING DATE: April 6, 1994

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2316 base pairs
(B) TYPE: nucleic acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATCCTGAAGG	CAGAGAGCGG	CTCCGACAC	GGCTATGACG	TCACCGATCC	CGCCGTAGTG	180
GACCCGGAGC	GCGGCCGCCC	TGAAGGGCTG	GCCGCGGTGT	CCAAGGCGGC	CCGCGGTGCC	240
GGCATGGCG	TGCTGATCGA	CATCGTCCG	AACCACGTGG	GCGTGGCGTC	CCGCGGCAG	300
AACCCGTGGT	GGTGGTCGCT	GCTCAAGGAA	GGGCGCGGGT	CGCCCTACGC	CGTGGCGTTC	360
GACGTCGACT	GGGACCTGGC	GGGGGGCCGC	ATCCGGATCC	CCGTCCTGGG	CAGCGACGAC	420
GATCTGGACC	AGCTCGAAAT	CAAGGACCGG	GAGCTGCGGT	ACTACGACCA	CCGCTTCCC	480
CTGGCCGAGG	GCAGCTACCG	GGACGGCGAC	TCCCCCGCAGG	ACGTCCACGG	CCGGCAGCAC	540
TACGAACTCA	TCGGCTGGCG	GCGCGCCGAC	AATGAACTGA	ACTACCGCCG	GTTCTTCGCG	600
GTGAACACGC	TCGCCGGCAT	CCGGGTGGAG	GTGCCGCCGG	TCTTCGATGA	AGCGCACCAAG	660
GAGGTGGTGC	GCTGGTTCCG	TGCGGGCTC	GCCGACGGGC	TGCGGATCGA	CCACCCGGAC	720
GGCCTGCCG	ATCCCGAGGG	GTATTGAAAG	CGGCTCCGTG	AGGTCAACCGG	GGGCGCGTAC	780
CTGCTCATCG	AAAAGATCCT	CGAGCCGGGC	GAACAGTTGC	CGGCCAGCTT	CGAGTGCAGAA	840
GGCACCAACG	GCTACGACGC	CCTCCGGAT	GTGACAGGG	TCTTCGTTGA	CCCGCGGGGA	900
CAGGTGCCGC	TGGACCGTCT	GGACGCACGG	CTGGCGGGCG	GTGCCGCCGGC	CGACTACGAG	960
GACATGATCC	GGGGGACCAA	GCGCCGGATC	ACCGACGGCA	TCCTGCACTC	CGAGATCCTG	1020
CGCCTTGCCA	GGCTGGTGCC	CGAGCAGACC	GGAAATCCCG	GGGAGGGCGC	CGCGGATGCG	1080

5 ATCGCGGAGA TCATCGCGGC CTCCCCGGTC TACCGGTCCCT ATCTTCCCGA GGGCGCGGAG 1140
 ATCTGAAGG AGGCCTGCAG CCTCGCCGG CGGAGGCAGTC CGGAACACTGGG CCAGACCGTC 1200
 CAGCTGCTGC AGCGCCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
 ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320
 CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
 TTTCACGTCC GGATGGCCCG CCGGCAGGCC GAACCTCCGC TCTCCATGAC CACCTGAGC 1440
 ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
 10 GCGCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
 CCGCTCTCCA CGCTGCTCTG GCAGGCAGATT GCGGGGGCAT GGCGGGCCAG CGGGGAACGGC 1620
 CTTCAGTCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCGAG CTGGACCGAT 1680
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 GAACGGATTAA GGGCCTTGGA CCAGTGGAC GCGGGCCACC GTCCGGACTC CTTCCAGGAC 1980
 GAGGGCGCTCA AGCTGCTGGT CACCTCGAGG GCGCTCGGGC TGCGGGGGAA CGGGCCCGAG 2040
 CTCTTCACCG GCTACCGCCC CGTGCATGCC AGGGGGGGCG CGCGCCGGCA CCTGGTGGCG 2100
 TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
 CAGTCGGGCG GCTGGCGGGG CACCGCCGTC GAGCTTGAAG CGGCCATGAC GGACGAACGT 2220
 ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCG GGCCTACCCG 2280
 20 GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 772

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
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 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 45 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 50 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 5 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 10 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 360 365 370
 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 15 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 20 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 445 450 455
 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 25 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 495 500 505 510
 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 30 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 35 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 40 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 45 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 735 740 745
 50 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 Pro Ala Thr Gly Gly Lys Ser
 770

55 (4) INFORMATION FOR SEQ ID NO:3:
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2325 base pairs

(B) TYPE:nucleic acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTCAC ACTCTTCGAC	60
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	GTCCTGACTG CCGAGCAGGG CCTCGACCTCG GGGTACGACG TCACCGATCC CTCCGCCGTC	180
10	GACCCGAAC GCGGGGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGGCCCGCG	240
	GGCATGGCG TGCTGATCGA CATCGTGCC ACCACAGTGG GCGTCGCGAC GCCGGCGCAG	300
	AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCCTTC	360
	GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCAGCAGT	420
	GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG	480
15	CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCCGGG ATGTCCACGC CCGGCAGCAC	540
	TACGAGCTCA TCGGCTGGCG CCGCGCCGAA AACGAGCTGA ACTACGCCG CTTTTCGCG	600
	GTGACACGC TCGGCGCGT CCGCGTGGAA ATCCCCCGC TCTTCGACCA GGCACACCAAG	660
	GAGGTGGTGC GCTGGTTCG CGAGGACCTT CGGGACGGCC TGCGGATCGA CCACCCGGAC	720
	GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGGCTTAC	780
	CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA	840
20	GGCACCAACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC	900
	CAGGAACCGC TGGACGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAAG	960
	GACATGATCC GCGGAACCAA CGCCCGGATC ACCGACGGTA TCCTGCACTG GGAGATCCTG	1020
	CGGCTGGGCC GGCTGGTCC GGGCGACGCC AACGTTCAA TCGACGCCGG AGCCGACGCT	1080
	CTCGCCGAAA TCATCGCCGC CTTCCCGTC TACCGCACCT ACCTGCGGGA GGGCGCCGAG	1140
	GTCTCGAAGG AGGCGTGCAG GCTTGCAGCG CGTAGGCAGGC CGGAACCTCGA CCAGGCCATC	1200
	CAGGCTCTGC AGCCGCTGCT GCTGGACACAG GACCTCGAGC TTGCCCCGGC CTTCCAGCAG	1260
25	ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCG CTACAACCGC	1320
	CTGGGCACCC TCACGGAAGT GGGGCGCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG	1380
	TTCCACGCCC GGCTGGCACG CCGGCAGGCC GAGCTCCGC TGTCCATGAC GACGCTGAGC	1440
	ACGGACGACA CCAAGCCGAG CGAGGACACCC CGAGCAAGGA TTTCGGTCA TTCCGAGGTT	1500
	GCGGGTACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGGC GCCGGACGGC	1560
	CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCGGGCGCCT GGCCCGCCAG CGGGGAACGC	1620
30	CTGCAGTACT ACGCGCTGAA GGGCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT	1680
	CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCGCGGTGCG ACGCCGTGTT CGACAATCCC	1740
	GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCTGG AGCCGTAACGG AGCTTCGAAC	1800
	TCCCTCGCCG CCAAGCTCGT GCAGCTGAC ATGCCCGGC TCCCGGACGT CTACCAAGGGC	1860
	ACGGAGTTCT GGGACGGGTG GCTGACGGAC CGGGACAACC GGGCGCCGGT CAGCTTCGAC	1920
	GACCCGCCGCG CCGCGCTTGGA GCAGCTGGAT GCGGGCGACC TTCCCGCTC ATTACCGAT	1980
35	GAGCGGACGA AGCTGCTAGT GACGTGCGCG GCGCTGCGGC TGCGCCGGGA CGTCCGGAG	2040
	CTGTTCACGG GGTACGGCC GGTCTCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG	2100
	TTCGACCGCG GCACCGCCGC GGGGCCGGGT GCATTGACCC TCGCCACGGG GCTTCCTAC	2160
	GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCGCTCG AACTTAACAC CGCCATGAAA	2220
	GACGAACCTGA CCGGTGCCGG CTTCGGACCG GGGGCACTGA AGATCGCCGA CATTTCCGG	2280
	TCGTTCCCCG TTGCGCTGCT GGTGCCGAG ACAGGAGGAG AGTCA	2325

40

(5) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 775

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr	
1	5 10 15	
	Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp	
50	20 25 30	
	Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly	
35	40 45 50	
	Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu	
	55 60 65	
55	Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu	
	70 75 80 85	

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 90 95 100
 5 Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 140 145 150
 10 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 155 160 165 170
 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 15 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gln Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 20 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300
 25 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 30 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 35 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu GLY
 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 40 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 45 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 545 550 555 560
 50 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 55 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625

Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 5 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 10 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 700 705 710
 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 15 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
 750 755 760 765
 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
 770 775

- 20 (6) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:14 base pairs
 - (B) TYPE:nucleic acid
 - (C) STRANDEDNESS:single
 - (D) TOPOLOGY:unknown
 - (ii) MOLECULE TYPE:other nucleic acid
 - (A) probe
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCNGARTGGG ARAA

14

- 35 (7) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:14 base pairs
 - (B) TYPE:nucleic acid
 - (C) STRANDEDNESS:single
 - (D) TOPOLOGY:unknown
 - (ii) MOLECULE TYPE:other nucleic acid
 - (A) probe
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACNGARTTYT GGGA

14

- (8) INFORMATION FOR SEQ ID NO:7:
- 50 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH:17 base pairs
 - (B) TYPE:nucleic acid
 - (C) STRANDEDNESS:single
 - (D) TOPOLOGY:unknown
 - 55 (ii) MOLECULE TYPE:other nucleic acid
 - (A) primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5 GTAAAACGAC GGCCAGT

17

(9) INFORMATION FOR SEQ ID NO:8:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:17 base pairs
- (B) TYPE:nucleic acid
- (C) STRANDEDNESS:single
- (D) TOPOLOGY:unknown

15 (ii) MOLECULE TYPE:other nucleic acid

- (A) probe

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTYGAYGTNG AYTGGGA

17

20 (10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:14 base pairs
- (B) TYPE:nucleic acid
- (C) STRANDEDNESS:single
- (D) TOPOLOGY:unknown

(ii) MOLECULE TYPE:other nucleic acid

- (A) probe

30 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:9:

ACNGARTTYT GGGGA

14

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:2936 base pairs
- (B) TYPE:nucleic acid
- (C) strandedness:double
- (D) TOPOLOGY:linear

(ii) MOLECULE TYPE:genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:Rhizobium sp.
- (B) INDIVIDUAL ISOLATE:M-11 (FERM BP-4130)

(ix) FEATURE:

- (A) NAME/KEY:5' UTR
- (B) LOCATION:1..564
- (C) IDENTIFICATION METHOD:E
- (A) NAME/KEY:mat peptide
- (B) LOCATION:565..2880
- (C) IDENTIFICATION METHOD:S
- (A) NAME/KEY:3' UTR
- (B) LOCATION:2881..2936
- (C) IDENTIFICATION METHOD:E

50 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:10:

CGTGCTCTAC	TTCAACGCGC	ACGACGGCGA	CGTCGTGTTG	AAGCTCCCGT	CGGATGAATA	60
CGCCCCGGCC	TGGGACGTCA	TCATCGACAC	CGCCGGCGCG	GGTGCCGATT	CCGAACCCGT	120
GCAGGGCTGGC	GGCAAACCTCA	CCGTGGCAGC	GAAATCGCTC	GTGGTGCTCC	GTGCCAACAG	180
CGCCCCGGAG	GAGGAACCGG	ACCAACTCGGT	GGCCGCCTCC	CTCGCAGCGC	TGACGCAGAC	240
55 TGCGACCGCC	GAAACCGCGG	CGCTCACCGC	CCCCACCGTT	CCGGAGCCGA	GGAAGACCAA	300

	GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCACGAG GCGGCGCCGA AGCCGGAAGA	360
5	GAAGGCTCCC GACGAGGCCGG CGGCAGAGCC GGAAGAGGCT GTTCCGACG AGGCGGCCGGC	420
	GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA	480
	CGAGGCCGGCG CGCAAGCCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GCGAGCGCC	540
	AGGCAAGCAG GGCGGGACGG GCTC	564
	ATG AGG ACA CCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC	612
	Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe	
	1 5 10 15	
10	ACG CTG TTT GAT GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG	660
	Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly	
	20 25 30	
	GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC	708
15	Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser	
	35 40 45	
	GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC	756
	Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg	
	50 55 60	
	GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC	804
	Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala	
20	65 70 75 80	
	GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG	852
	Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala	
	85 90 95	
	TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC	900
	Ser Pro Pro Gln Asn Pro Trp Trp Ser Leu Leu Lys Glu Gly Arg	
25	100 105 110	
	GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG	948
	Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly	
	115 120 125	
	GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG	996
	Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln	
30	130 135 140	
	CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG	1044
	Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro	
	145 150 155 160	
	CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC	1092
	Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His	
35	165 170 175	
	GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA	1140
	Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu	
	180 185 190	
	CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG	1188
	Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg	
	195 200 205	
40	GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC	1236
	Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg	
	210 215 220	
	TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC	1284
	Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp	
	225 230 235 240	
45	GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG ATC CTC GAG CCG GGC GAA CAG	1332
	Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr	
	245 250 255	
	GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG	1380
	Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln	
	260 265 270	
50	TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC	1428
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu	
	275 280 285	
	GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG	1476
	Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu	
	290 295 300	
55	GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GAC TAC GAG	1524

Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
 5 305 310 315 320
 GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC 1572
 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 325 330 335 340
 TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT 1620
 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
 10 340 345 350 355
 CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC 1668
 Pro Gly Glu Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
 355 360 365 370
 CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716
 Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
 375 380 385 390
 15 GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764
 Ala Cys Asp Leu Ala Ala Arg Arg Pro Glu Leu Gly Gln Thr Val
 385 390 395 400
 CAG CTG CTG CAG CCG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812
 Gln Leu Leu Gln Pro Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
 405 410 415 420
 20 AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860
 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430 435
 ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val GLY
 435 440 445 450
 25 GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
 Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
 450 455 460 465
 ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
 Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 30 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495 500
 ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
 Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
 500 505 510 515
 35 ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
 Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
 515 520 525 530
 GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540 545
 40 GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
 545 550 555 560
 CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
 Pro Asp Pro Ala Phe Glu Ala Leu Ser Ala Val Val Asp Ser Ala
 565 570 575 580
 45 TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC 2340
 Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
 580 585 590 595
 CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG 2388
 Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 595 600 605 610
 50 CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG 2436
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 610 615 620 625
 GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC 2484
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
 625 630 635 640
 55 GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC 2532
 Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp

	645	650	655	
5	TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG	2580		
	Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu			
	660	665	670	
	CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG	2628		
	Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val			
	675	680	685	
10	CAT GCC AGG GGC CCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC	2676		
	His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly			
	690	695	700	
	GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA	2724		
	Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu			
	705	710	715	720
15	CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG	2772		
	Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met			
	725	730	735	
	ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG	2820		
	Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu			
	740	745	750	
20	TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA	2868		
	Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Val Pro Ala Thr			
	755	760	765	
	GGA GGC AAG TCA	2880		
	Gly Gly Lys Ser			
	770			
	TGACCGAGCC CAACGATGCG GCCAAGCCGG TGCAAGGGAGC GGGCGCTTC GATATC			2936

25

(12) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3084 base pairs
- (B) TYPE:nucleic acid
- (C) strandedness:double
- (D) TOPOLOGY:linear

30

(ii) MOLECULE TYPE:genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:Arthrobacter sp.
- (B) INDIVIDUAL ISOLATE:Q36 (FERM BP-4316)

35

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION:1..677
- (C) IDENTIFICATION METHOD:E
- (A) NAME/KEY: mat peptide
- (B) LOCATION:678..3002
- (C) IDENTIFICATION METHOD:S

40

- (A) NAME/KEY: 3'UTR
- (B) LOCATION:3003..3073
- (C) IDENTIFICATION METHOD:E

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:11:

	GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTGGTG	60
45	GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGGGGCG CGCGATCACG	120
	GACGTGAECT TCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG	180
	CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATGACA CCGCCGGTGA AGGGGCCGAC	240
	TCCAAGCCCG CGGACGCCGG AACCATCTG TCCGGTGCAG CCAAGTCGCT GGTGTTGCTT	300
	CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCG TGGCTGCTTC CCTGGCTGCA	360
	CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCCTGCCGT TCCCGAGCCG	420
50	GCCAAGACGA AGAACCGGGC CGCTGACCCG GTTGTGAAC CGGGCGAACCC GCGCGTTGCT	480
	GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAAACC GGCTGCGGAG	540
	CCTGGAAAT CCGCAGCGGA ACCTGGTGCAG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG	600
	GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGCG GCCACCTGAG GGCGGTCAAG	660
	CCCGCTGGGG AGGACGCG	677
55	ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC	725
	Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe	

	1	5	10	15	
5	ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC				773
	Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly				
	20	25	30		
	GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC				821
	Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser				
	35	40	45		
10	GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC				869
	Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg				
	50	55	60		
	GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG				917
	Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala				
	65	70	75	80	
15	GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG				965
	Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala				
	85	90	95		
	ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC				1013
	Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg				
	100	105	110		
20	CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG				1061
	Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly				
	115	120	125		
	GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG				1109
	Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln				
	130	135	140		
25	CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG				1157
	Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro				
	145	150	155	160	
	CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC				1205
	Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His				
	165	170	175		
30	GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG				1253
	Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu				
	180	185	190		
	CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC				1301
	Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg				
	195	200	205		
35	GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC				1349
	Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg				
	210	215	220		
	TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC				1397
	Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp				
	225	230	235	240	
	GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC				1445
	Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr				
40	245	250	255		
	GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG				1493
	Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln				
	260	265	270		
	CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GCA GGC TAC GAC GCC CTC				1541
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu				
45	275	280	285		
	GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG				1589
	Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu				
	290	295	300		
	GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG				1637
	Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Pro Ala Asp Tyr Gln				
50	305	310	315	320	
	GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC				1685
	Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His				
	325	330	335		
	TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT				1733
	Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val				
	340	345	350		

	TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC	1781
5	Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe	
	355 360 365	
	CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG	1829
	Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu	
	370 375 380	
	GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC	1877
10	Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile	
	385 390 395 400	
	CAG GCT CTG CAG CCG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG	1925
	Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg	
	405 410 415	
	CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC	1973
15	Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp	
	420 425 430	
	ACC GCG TTC CGC TAC AAC CGC CTG GCC ACC CTC ACG GAA GTG GGC	2021
	Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly	
	435 440 445	
	GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG	2069
20	Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg	
	450 455 460	
	CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC	2117
	Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser	
	465 470 475 480	
	ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC	2165
	Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val	
25	485 490 495	
	ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC	2213
	Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg	
	500 505 510	
	GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG	2261
30	Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln	
	515 520 525	
	GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC	2309
	Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr	
	530 535 540	
	GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT	2357
	Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp	
35	545 550 555 560	
	CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG	2405
	Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val	
	565 570 575	
	TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC	2453
	Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu	
40	580 585 590	
	CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG	2501
	Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln	
	595 600 605	
	CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG	2549
	Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp	
	610 615 620	
45	GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC	2597
	Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp	
	625 630 635 640	
	GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG	2645
	Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala	
	645 650 655	
50	TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG	2693
	Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu	
	660 665 670	
	CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC	2741
	Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val	
	675 680 685	
55	CTG GCC AGC GGG CCC GCC GCG CAC CTG CTC GCG TTC GAC CGC GGC	2789

5 Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
 690 695 700
 ACC GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC 2837
 Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
 705 710 715 720
 GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC 2885
 Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn
 725 730 735
 10 ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA 2933
 Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala
 740 745 750
 GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG 2981
 Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val
 755 760 765
 15 CCG CAG ACA GGA GGA GAG TCA 3002
 Pro Gln Thr Gly Gly Glu Ser
 770 775
 TGACGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCCT GGGCCCCGCA CGCTACGACG 3062
 TCTGGCGGCC C 3073

20 (13) INFORMATION FOR SEQ ID NO:12:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal fragment
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
 1 5 10 15
 30 Leu Phe Asp
 20

(14) INFORMATION FOR SEQ ID NO:13:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal fragment
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
 40 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 Leu Phe Asp
 20

45 (15) INFORMATION FOR SEQ ID NO:14:
 (i) SEQUENCE CHARACTERISTICS :
 (A) LENGTH: 21
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal fragment
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
 50 Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val Ile Ala Glu Val Ala Pro
 1 5 10 15
 Glu Trp Glu Lys
 20

(16) INFORMATION FOR SEQ ID NO:15:
(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 21
(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE:peptide
(v) FRAGMENT TYPE:internal fragment
(xi) SEQUENCE DESCRIPTION:SEQ ID NO

10

Leu Val Gln Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu
 1 5 10 15
 Phe Trp Asp Arg 20

15

(17) INFORMATION FOR SEQ ID NO:16:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20
(B) TYPE: amino acid
(C) TOPOLOGY: linear

20 (D) TOPOLOGY:linear
(ii) MOLECULE TYPE:peptide
(v) FRAGMENT TYPE:internal fragment
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:16:

Leu Val Gln Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu
 1 5 10 15
 Phe Trp Asp

1

File Tip Asp
20

(18) INFORMATION FOR SEQ ID NO:17:
(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 20
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal fragment
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu
 1 5 10 15
 Ala Gly Gly
 20

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45 Claims

- 50 1. A DNA encoding an enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher.

2. The DNA as claimed in claim 1, wherein said enzyme has the following physicochemical properties:

(1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and

(2) Isoelectric point (pi)
About 3.6-4.6 on isoelectrophoresis.

55 3. The DNA as claimed in claim 1, wherein said enzyme has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and

homologous amino acid sequences to thes amino acid sequences:

5 SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
1 5 10 15

10 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
20 25 30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
15 35 40 45 50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65

20 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu

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5	70	75	80	85
	Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro			
	90	95	100	
10	Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala			
	105	110	115	
15	Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu			
	120	125	130	135
	Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg			
20	140	145	150	
	Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp			
	155	160	165	170
25	Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg			
	175	180	185	
	Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu			
30	190	195	200	
	Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu			
	205	210	215	220
35	Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His			
	225	230	235	
	Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val			
40	240	245	250	255
	Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln			
	260	265	270	
45	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala			
	275	280	285	
	Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg			
50	290	295	300	305
	Leu Asp Ala Arg Leu Arg Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile			
	310	315	320	

5 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 10 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 345 350 355
 15 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 360 365 370
 20 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 25 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 395 400 405
 30 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 35 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 40 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 445 450 455
 45 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 50 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 55 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 495 500 505 510
 60 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 515 520 525
 65 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 70 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 75 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 55

5	565	570	575	
	Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro			
	580	585	590	595
10	His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro			
	600	605	610	
	Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr			
15	615	620	625	
	Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu			
	630	635	640	645
20	Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val			
	650	655	660	
	Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu			
25	665	670	675	680
	Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His			
	685	690	695	
30	Leu Val Ala Phe Asp Arg Gly Ala Gly Val Leu Ala Leu Ala Thr Arg			
	700	705	710	
	Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu			
35	715	720	725	730
	Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly			
	735	740	745	
40	Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val			
	750	755	760	765
	Pro Ala Thr Gly Gly Lys Ser			
45	770			
50				

SEQ ID NO:4

55	Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr		
	1	5	10
			15

5 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 10 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 15 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 20 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 25 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 30 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 155 160 165 170
 35 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 40 190 195 200
 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 45 205 210 215 220
 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 50 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

5	260	265	270
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala		
	275	280	285
10	Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg		
	290	295	300
	Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile		
15	310	315	320
	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu		
	325	330	335
20	Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly		
	345	350	355
	Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr		
25	360	365	370
	Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg		
	375	380	385
30	Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu		
	395	400	405
	Asp Thr Asp Leu Glu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val		
35	410	415	420
	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly		
	430	435	440
40	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp		
	445	450	455
	Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met		
45	460	465	470
	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg		
	480	485	490
50	Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg		
	495	500	505
			510

5 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 10 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 15 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 545 550 555 560
 20 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 25 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 30 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 35 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 40 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 45 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 650 655 660
 50 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Asp Arg Pro Glu
 665 670 675 680
 55 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 60 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 700 705 710
 65 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 70 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 75 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

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Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

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4. The DNA as claimed in claim 1, which has a base sequence selected from the group consisting of those
 as shown in the following SEQ ID NOS:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to these base sequences:

15 SEQ ID NO:1

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ATGAGGACAC CCGCTCGAC CTACCGCTG CAGATCAGGC GGGGTTTCAC GCTGTTTGAT 60
GCCGCCGAGA CCGTGCCTA CCTGAAGTCA CTCGGGTGG ACTGGATCTA CCTGTCGCC 120
20 ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTGC 180
GACCCGGAGC GCGGCGGCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240
GGCATGGCG TGCTGATCGA CATCGTGCCT AACACACGTGG GCGTGGCGTC GCCGCCGCAG 300
25 AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360
GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CGTCCTGGG CAGCGACGAC 420
GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCC 480
30 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC 540
TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600
GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA ACCGCACCAAG 660
35 GAGGTGGTGC GCTGGTCCG TGCAGGGCTC GCCGACGGGC TGCGGATCGA CCACCCGGAC 720
GGCCTGGCCG ATCCCGAGGG GTATTTGAAG CGGCTCCGTG AGGTCAACCGG GGGCGCGTAC 780
CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCAGAA 840
40 GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 900
CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGCG GTGCGCCGGC CGACTACGAG 960
GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
45 CGCCTTGCCA GGCTGGTGCC CGAGCAGACCC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080
ATCGCGGAGA TCATCGCGGC CTTCCGGTC TACCGGTCT ATCTTCCCGA GGGCGCGGAG 1140
ATCCTGAAGG AGGCCTGCGA CCTCGCCGGC CGGAGGCGTC CGGAACCTGGG CCAGACCGTC 1200
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5 CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
 ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320
 CTGGGAACGC TCACCGAGGT GGGCCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
 10 TTTCACGTCC GGATGGCCCCG CGGGCAGGCC GAACTCCCAGC TCTCCATGAC CACCCCTGAGC 1440
 ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
 GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
 15 CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCAGGGGCAT GGCCGGCCAG CGGGAACGC 1620
 CTTCAGTCCT ACGCCCTGAA AGCGGCGCAG GAAGCCGGGA ACTCGACCAG CTGGACCGAT 1680
 CCGGACCCGG CATTGAGGA GGCACCTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740
 20 GAGGTGCGTG CGGAACCTTGA GGCCCTGGTG GGCCCTCCTTG CGCCGCACGG TGCGTCCAAC 1800
 TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGCG TTCCGGACGT GTACCAGGGC 1860
 ACCGAGTTCT GGGACAGGTG GCTGACCGAT CCGGACAACC GGCGCCCTT CAGCTTCGCC 1920
 25 GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
 GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TGCGCGGAA CGGGCCCGAG 2040
 CTCTTCACCG GCTACCGCCC CGTGCATGCC AGGGGCCCCG CCGCCGGGCA CCTGGTGGCG 2100
 30 TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCTA CGGGCTGGAA 2160
 CAGTCGGCG GCTGGCGGG A CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAAC TG 2220
 ACCGGCTCCA CTTTCGGGCC GGGACCGGCG GCGCTGTCAG AAGTCTTCCG GGCCTACCCG 2280
 35 GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA

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SEQ ID NO:3

5 ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTAC ACTCTTCGAC 60
GCGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
10 GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGGCCGCG 240
GGCATGGCG TGCTGATCGA CATCGTGCCC AACACACGTGG CGCTCGCGAC GCCGGCGCAG 300
AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCAGTC 360
15 GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCAGGT ACTACGACCA CCGATTCCCG. 480

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55

5 CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGGGG ATGTCCACGC CCGGCAGCAC 540
 TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTCGCG 600
 GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCG TCTTCGACGA GGCACACCAG 660
 10 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TGCGGATCGA CCACCCGGAC 720
 GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGCCTTAC 780
 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
 15 GGCACACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGGC 900
 CAGGAACCGC TGGACCGGCT TGACCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960
 GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
 20 CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTCAA TCGACGCCGG AGCCGACGCT 1080
 CTCGCCAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
 GTCCTGAAGG AGGCGTGCAG GCTTGCCGCG CGTAGGCGGC CGGAACCTCGA CCAGGCCATC 1200
 25 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCCGGCG CTTCCAGCAG 1260
 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTCCG CTACAACCGC 1320
 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380
 30 TTCCACGCC GGCTGGCACG CGGGCAGGCC GAGCTTCCG TGTCATGAC GACGCTGAGC 1440
 ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
 GCGGGTGAAT GGGAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
 35 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCGCCAG CGGGAACGC 1620
 CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
 40 CCGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTG ACGCCGTGTT CGACAATCCC 1740
 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTGAAC 1800
 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGCG TCCCGGACGT CTACCAGGGC 1860
 45 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CGGGACAACC GGCGGCCGTT CAGCTTGCAC 1920
 GACCGCCGCG CGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
 GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGGC TGCGCCGGGA CCGTCCGGAG 2040
 50 CTGTTACGG GGTACCGGCC GGTCCCTGGCC AGCGGGCCCG CGGGCGGCCA CCTGCTCGCG 2100
 TTCGACCGCG GCACCGCGGC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTG AACTTAACAC CGCCATGAAA 2220

GACGAACTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280
 TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325

5

5. The DNA as claimed in claim 4, wherein one or more bases in SEQ ID NO:1 or 3 are replaced with other bases by means of degeneracy of genetic code without alternating the amino acid sequence of the following SEQ ID NO:2 or 4:

10

SEQ ID NO:2

15	Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr				
1	5	10	15		
20	Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp	20	25	30	
25	Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly	35	40	45	50
30	Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu	55	60	65	
35	Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu	70	75	80	85
40	Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro	90	95	100	
45	Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala	105	110	115	
50	Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu	120	125	130	135
55	Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg	140	145	150	
60	Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp	155	160	165	170
65	Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg	175	180	185	

55

5 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 10 205 210 215 220
 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 15 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 20 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 25 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 30 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 35 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 345 350 355
 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 40 360 365 370
 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 45 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 50 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly

5	430	435	440
	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu		
	445	450	455
10	Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met		
	460	465	470
	475		
	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg		
15	480	485	490
	Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg		
	495	500	505
20	510		
	Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp		
	515	520	525
	Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr		
25	530	535	540
	Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro		
	545	550	555
30	560		
	Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp		
	565	570	575
	Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro		
35	580	585	590
	595		
	His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro		
40	600	605	610
	Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr		
	615	620	625
45	Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu		
	630	635	640
	645		
	Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val		
50	650	655	660
	Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu		
	665	670	675
	680		

Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 5 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 10 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 15 735 740 745
 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 20 Pro Ala Thr Gly Gly Lys Ser
 770

25

30 SEQ ID NO:4
 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 35 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 40 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 45 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 50 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 55 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu

5	120	125	130	135
	Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg			
	140	145	150	
10	Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp			
	155	160	165	170
	Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg			
15	175	180	185	
	Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu			
	190	195	200	
20	Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu			
	205	210	215	220
	Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His			
25	225	230	235	
	Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val			
	240	245	250	255
30	Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln			
	260	265	270	
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala			
35	275	280	285	
	Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg			
	290	295	300	305
40	Leu Asp Ala Ser Leu Arg Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile			
	310	315	320	
45	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu			
	325	330	335	340
	Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly			
50	345	350	355	
	Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr			
	360	365	370	

5 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 10 395 400 405
 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 15 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 20 445 450 455
 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 25 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 30 495 500 505 510
 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 35 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 40 545 550 555 560
 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 45 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 50 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr

	615	620	625	
5	Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu			
	630	635	640	645
10	Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr			
	650	655	660	
	Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu			
15	665	670	675	680
	Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His			
	685	690	695	
20	Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu			
	700	705	710	
	Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr			
25	715	720	725	730
	Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe			
	735	740	745	
30	Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala			
	750	755	760	765
	Leu Leu Val Pro Gln Thr Gly Gly Glu Ser			
35	770	775		

40 6. The DNA as claimed in claim 1, which has the base sequence as shown in the following SEQ ID NO:10 or 11:

45 SEQ ID NO:10:

CGTGCTCTAC TTCAACCGCGC ACGACGGCGA CGTCGTGTTA AAGCTCCCGT CGGATGAATA	60
CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT	120
50 GCAGGCTGGC GGCAAACCTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCACAG	180
CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC	240
TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA	300
55 GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCAGCGAG CGGGCGCCGA AGCCGGAAGA	360
GAAGGCTCCC GACGAGGCCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCCGGC	420

5 GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CGGAAAGAGG CTGCTTCCGA 480
 CGAGGCCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC 540
 AGGCAAGCAG GGCGGGACGG GCTC 564
 10 ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC 612
 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
 1 5 10 15
 15 ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG 660
 Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
 20 25 30
 20 GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC 708
 Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
 35 40 45
 25 GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
 Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
 50 55 60
 30 GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
 65 70 75 80
 35 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 40 TCG CCG CCG CAG AAC CCG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
 Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 45 GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
 Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 50 GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG 996
 Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln

5	130	135	140
	CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG 1044		
	Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro		
10	145	150	155
	CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC 1092		
	Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His		
15	165	170	175
	GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA 1140		
	Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu		
20	180	185	190
	CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG 1188		
	Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg		
25	195	200	205
	GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC 1236		
	Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg		
30	210	215	220
	TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC 1284		
	Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp		
35	225	230	235
	240		
	GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC 1332		
	Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr		
40	245	250	255
	260		
	GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG 1380		
	Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln		
45	265	270	
	TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC 1428		
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu		
50	275	280	285
	GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG 1476		

5 Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
 290 295 300
 GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG 1524
 10 Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
 305 310 315 320
 GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC 1572
 15 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 325 330 335
 TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT 1620
 20 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
 340 345 350
 CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC 1668
 25 Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716
 30 Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
 370 375 380
 GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764
 35 Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
 385 390 395 400
 CAG CTG CTG CAG CCG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812
 40 Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
 405 410 415
 AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860
 45 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
 50 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445

5 GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
 Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
 450 455 460
 10 ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
 Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 15 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 20 ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
 Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
 500 505 510
 25 ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
 Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
 515 520 525
 30 GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 35 GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
 545 550 555 560
 40 CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
 Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
 565 570 575
 45 TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC 2340
 Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
 580 585 590
 50 CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG 2388
 Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln

5 595 600 605
 CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG 2436
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 10 610 615 620
 GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC 2484
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
 15 625 630 635 640
 GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC 2532
 Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp
 20 645 650 655
 TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG 2580
 Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu
 25 660 665 670
 CCG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628
 Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
 30 675 680 685
 CAT GCC AGG GGC CCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676
 His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly
 35 690 695 700
 GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724
 Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu
 40 705 710 715 720
 CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772
 Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met
 45 725 730 735
 ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820
 Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
 50 740 745 750
 TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868

Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr

755 760

765

5 GGA GGC AAG TCA

2880

Gly Gly Lys Ser

770

10 TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936

15

SEQ ID NO:11

20 GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GC GGCTTCGG CCGTTGGTG 60

GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120

GACGTGAAC T C C T G C T G T A C T T C A A C G C C C A C G A C G G C G A C G T C G A G T T C A C G C T G C C G 180

25 CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240

TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGGG CCAAGTCGCT GGTGTTGCTT 300

CGCGCCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360

30 CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCCTGCCGT TCCCAGGCCG 420

GCCAAGACGA AGAACGCCGG CGCTGACCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480

45 GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAAACC GGCTGCGGAG 540

CCTGC GAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600

GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGCG G C C A C C T G A G G G C G G T C A A G 660

40 CCCGCTGGGG AGGACGC 677

ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe

45 1 5 10 15

ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773

Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly

50 20 25 30

GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC 821

Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser

55 35 40 45

5 GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
 Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
 50 55 60
 10 GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
 65 70 75 80
 15 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 20 ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
 Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 25 CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
 Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 30 GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
 Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 130 135 140
 35 CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
 Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 145 150 155 160
 40 CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
 Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
 165 170 175
 45 GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
 Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 180 185 190
 50 CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg

5	195	200	205	
	GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC 1349			
	Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg			
10	210	215	220	
	TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC 1397			
	Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp			
15	225	230	235	240
	GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC 1445			
	Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr			
20	245	250	255	
	GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG 1493			
	Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln			
25	260	265	270	
	CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC 1541			
	Leu Pro Ala Ser Phe Glu Cys Gly Thr Thr Gly Tyr Asp Ala Leu			
30	275	280	285	
	GCC GAC GTC GAC CCG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG 1589			
	Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu			
35	290	295	300	
	GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG 1637			
	Asp Arg Leu Asp Ala Ser Leu Arg Gly Glu Pro Ala Asp Tyr Gln			
40	305	310	315	320
	GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC 1685			
	Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His			
45	325	330	335	
	TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT 1733			
	Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val			
50	340	345	350	
	TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC 1781			

5 Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829
 10 Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
 370 375 380
 GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC 1877
 15 Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
 385 390 395 400
 CAG GCT CTG CAG CCG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925
 20 Gln Ala Leu Gln Pro Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
 405 410 415
 CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973
 25 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
 30 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
 35 Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
 450 455 460
 CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
 40 Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
 45 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
 50 Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
 500 505 510

5 GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
 Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
 515 520 525
 10 GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 15 GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
 545 550 555 560
 20 CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
 Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
 565 570 575
 25 TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC 2453
 Phe Asp Asn Pro Ala Val Gin Ala Glu Val Glu Ala Leu Val Glu Leu
 580 585 590
 30 CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG 2501
 Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 595 600 605
 35 CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG 2549
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 610 615 620
 40 GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC 2597
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
 625 630 635 640
 45 GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG 2645
 Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
 645 650 655
 50 TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG 2693
 Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu
 55

5	660	665	670
	CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CCG CCG GTC 2741		
	Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val		
10	675	680	685
	CTG GCC AGC GGG CCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC 2789		
	Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly		
15	690	695	700
	ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC 2837		
	Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr		
20	705	710	715
	720		
	GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC 2885		
	Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn		
25	725	730	735
	ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA 2933		
	Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala		
30	740	745	750
	GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG 2981		
	Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val		
35	755	760	765
	CCG CAG ACA GGA GGA GAG TCA 3002		
	Pro Gln Thr Gly Gly Glu Ser		
40	770	775	
	TGACGCACAC CTACCCGCAG GAAGCCGCGA AACCCGTCTT GGGCCCCGCA CGCTACGACG 3062		
	TCTGGGGGCC C 3073		
45			

- 50 7. The DNA as claimed in claim 1, which is derived from a microorganism selected from the group consisting of those of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curtobacterium*, *Mycobacterium* and *Terrabacter*.
8. A replicable recombinant DNA containing the DNA of claim 1 and a self-replicable vector.
- 55 9. The replicable recombinant DNA as claimed in claim 8, wherein said DNA encodes an enzyme having the following physicochemical properties:
- (1) Molecular weight

About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
 (2) Isoelectric point (pI)
 About 3.6-4.6 on isoelectrophoresis.

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10. The replicable recombinant DNA as claimed in claim 8, wherein said DNA encodes an enzyme having an amino acid sequence selected from the group consisting of those as shown in SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous base sequences to these amino acid sequences:

10

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

15

1 5 10 15

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp

20

20 25 30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly

35 40 45 50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu

25

55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu

30

70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro

90 95 100

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5 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 10 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 15 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 20 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 25 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 30 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 35 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 40 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 45 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 50 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala

5	345	350	355
	Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr		
	360	365	370
10	Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg		
	375	380	385
	390		
	Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu		
15	395	400	405
	Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val		
	410	415	420
20	425		
	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly		
	430	435	440
	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu		
25	445	450	455
	Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met		
	460	465	470
30	475		
	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg		
	480	485	490
	Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg		
35	495	500	505
	510		
	Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp		
	515	520	525
40	Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr		
	530	535	540
	Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro		
45	545	550	555
	560		
	Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp		
	565	570	575
	Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro		
50	580	585	590
	595		

His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 5 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 10 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 15 630 635 640 645
 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 20 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 25 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 30 685 690 695
 Leu Val Ala Phe Asp Arg Gly Ala Gly Val Leu Ala Leu Ala Thr Arg
 35 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 40 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 45 735 740 745
 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 50 750 755 760 765
 Pro Ala Thr Gly Gly Lys Ser
 55 770

SEQ ID NO:4

5 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp

10 20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly

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5	35	40	45	50
	Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu			
	55	60	65	
10	Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu			
	70	75	80	85
	Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro			
15	90	95	100	
	Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala			
	105	110	115	
20	Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu			
	120	125	130	135
	Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg			
25	140	145	150	
	Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp			
	155	160	165	170
30	Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg			
	175	180	185	
	Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu			
35	190	195	200	
	Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu			
	205	210	215	220
40	Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His			
	225	230	235	
	Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val			
45	240	245	250	255
	Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln			
50	260	265	270	
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala			
	275	280	285	

5 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 10 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 15 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 20 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 25 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 30 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 35 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 40 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 45 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 50 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr

5	530	535	540	
	Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro			
10	545	550	555	560
	Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp			
	565	570	575	
15	Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro			
	580	585	590	595
	Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro			
20	600	605	610	
	Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr			
	615	620	625	
25	Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu			
	630	635	640	645
	Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr			
30	650	655	660	
	Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu			
	665	670	675	680
35	Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His			
	685	690	695	
	Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu			
40	700	705	710	
	Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr			
	715	720	725	730
45	Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe			
	735	740	745	
	Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala			
50	750	755	760	765
	Leu Leu Val Pro Gln Thr Gly Gly Glu Ser			
	770	775		

11. The replicable recombinant DNA as claimed in claim 8, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to those base sequences:

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10

SEQ ID NO:1

-ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTGAT 60
 GCCGCCGAGA CCGTGCCTA CCTGAAGTCA CTCGGGTGG ACTGGATCTA CCTGTCGCC 120
 ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180
 15 GACCCGGAGC GCGGCGGCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CGCGGGTGC 240
 GGCATGGGCG TGCTGATCGA CATCGTGCCTG ACCACAGTGG GCGTGGCGTC GCCGCCGCAG 300
 AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360
 20 GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420
 GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480
 25 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACgtCCACGG CGGCAGCAC 540
 TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600
 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660
 30 GAGGTGGTGC GCTGGTTCGG TCGGGGGCTC GCCGACGGC TGCGGATCGA CCACCCGGAC 720
 GGCCTGGCCG ATCCCAGGG GTATTGAAAG CGGCTCCGTG AGGTCAACCGG GGGCGCGTAC 780
 CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCAGAA 840
 35 GGCACCACCG GCTACGACGC CCTCGCGGAT GTGACAGGG TCTTCGTGGA CCCGCGGGGA 900
 CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCGGC GTGCGCCGGC CGACTACGAG 960
 GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
 40 CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080
 ATCGCGGAGA TCATCGCGGC CTTCCCGTC TACCGGTCT ATCTTCCCGA GGGCGCGGAG 1140
 ATCCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACGTGGG CCAGACCGTC 1200
 45 CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
 ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCGG CTACAACCGG 1320

50

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5 CTGGGAACGC TCACCGAGGT GGGGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
 TTTCACGTCC GGATGGCCCG CCGGCAGGCC GAACTCCCAGC TCTCCATGAC CACCCCTGAGC 1440
 ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
 GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
 10 CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCAGGGCAT GGCCGGCCAG CGGGGAACGC 1620
 CTTCAGTCCT ACGCCCTGAA AGCGGCGCAG GAAGCCGGGA ACTCGACCAAG CTGGACCGAT 1680
 CGGGACCCGG CATTGAGGA GGCACTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740
 15 GAGGTGGGTG CGGAACATTGA GGCCCTGGTG GGCCCTCCCTG CGCCGCACGG TGGCTCAAAC 1800
 TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGCG TTCCGGACGT GTACCAGGGC 1860
 ACCGAGTTCT GGGACAGGTC GCTGACCGAT CGGGACAAAC CGCCGCCCTT CAGCTTCGCC 1920
 20 GAACGGATTA GGGCCTTGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
 GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TGCGGCGGAA CGGGCCCGAG 2040
 CTCTTCACCG GCTACCGCCC CGTGCATGCC AGGGGCCCCG CGCCCGGGCA CCTGGTGGCG 2100
 25 TTCGACCGCG GCGCCGGGG AGTGGTGGCG CTTGCCACCC GGCTCCCTA CGGGCTGGAA 2160
 CAGTCGGCG GCTGGCGGG ACCCCCGTC GAGCTTGAAG CGCCCATGAC GGACGAAC 2220
 ACCGGCTCCA CTTTCGGGCC GGGACCGCG GCGCTGTCAG AAGTCTTCCG GGCTACCCG 2280
 30 GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

35

SEQ ID NO:3

40 ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTAC ACTCTTCGAC 60
 CGGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
 GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
 45 GACCCCGAAC GCGGCGGGCC GGAGGGCTC GCGGCGGTTT CCAAGGGCGC CCGCGCCGCG 240
 GGCATGGCG TGCTGATCGA CATCGTGCC ACCACGTGG GCGTCGCGAC GCCGGCGCAG 300
 AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
 50 GACGTGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
 GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
 55 CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCCGG ATGTCCACGC CGGGCAGCAC 540
 TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600

5 GTGAAACACGC TCGCCGGCGT CCCCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCAAG 660
 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGGCC TGCGGATCGA CCACCCGGAC 720
 GGCCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGGCCTTAC 780
 10 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
 GGCACCACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGC 900
 CAGGAACCGC TGGACCGGCT TGACGCGTCC CTGCGTGGCG GCGAGCCGC CGACTACCAG 960
 15 GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
 CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTCAA TCGACGCCGG AGCCGACGCT 1080
 CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
 20 GTCCTGAAGG AGGCGTGCAG GCTTGCCGCG CGTAGGCCGC CGGAACCTCGA CCAGGCCATC 1200
 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCCGGCG CTTCCAGCAG 1260
 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCG CTACAACCGC 1320
 25 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCCGGACGAG 1380
 TTCCACGCCCG GGCTGGCACG CCGGCAGGCC GAGCTTCCGC TGTCCATGAC GACGCTGAGC 1440
 ACGCACGACA CCAAGGCCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
 30 GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCGCCT GGCCCGCCAG CGGGAACGC 1620
 CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
 35 CGGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTG ACGCCGTGTT CGACAATCCC 1740
 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGCG TCCCGGACGT CTACCAGGGC 1860
 40 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920
 GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTTACCGAT 1980
 45 GAGCGGACGA AGCTGCTAGT GACGTGCGGC GCGCTGCGGC TGCGCCGGGA CGTCCGGAG 2040
 CTGTTCACGG GGTACCGGCC GGTCCCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100
 TTCGACCGCG GCACCGCGGC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
 50 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCGCTCG AACTTAACAC CGCCATGAAA 2220
 GACGAACCTGA CCGGTGCCGG CTTCGGACCG GGGCGAGTGA AGATCGCCGA CATCTTCCGG 2280
 TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325

12. The replicable recombinant DNA as claimed in claim 11, wherein one or more bases in SEQ ID NOs:1 and 3 are replaced with other bases by means of degeneracy of genetic code without altering their corresponding amino acid sequences of the following SEQ ID NOs:2 and 4 in this order:

5

SEQ ID NO:2

10	Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr			
1	5	10	15	
15	Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp			
20	20	25	30	
25	Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly			
30	35	40	45	50
35	Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu			
40	55	60	65	
45	Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu			
50	70	75	80	85
55	Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro			
60	90	95	100	
65	Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala			
70	105	110	115	
75	Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu			
80	120	125	130	135
85	Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg			
90	140	145	150	
95	Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp			
100	155	160	165	170
105	Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg			
110	175	180	185	
115	Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu			
120	50			

55

5	190	195	200
	Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu		
205	210	215	220
10	Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His		
	225	230	235
	Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val		
15	240	245	250
	255		
	Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln		
	260	265	270
20	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala		
	275	280	285
	Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg		
25	290	295	300
	305		
	Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile		
	310	315	320
30	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu		
	325	330	335
	340		
35	Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala		
	345	350	355
	Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr		
40	360	365	370
	Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg		
	375	380	385
	390		
45	Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu		
	395	400	405
	Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val		
50	410	415	420
	425		
	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly		
	430	435	440

5 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 445 450 455
 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 10 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 15 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 495 500 505 510
 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 20 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 25 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 30 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 35 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 40 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 45 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 50 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His

	685	690	695
5	Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg		
	700	705	710
10	Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu		
	715	720	725
15	Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly		
	735	740	745
20	Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val		
	750	755	760
	Pro Ala Thr Gly Gly Lys Ser		
25	770		

SEQ ID NO:4

30	Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr		
1	5	10	15
35	Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp		
	20	25	30
40	Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly		
	35	40	45
45	Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu		
	55	60	65
50	Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu		
	70	75	80
55	Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro		
	90	95	100
60	Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala		
	105	110	115
65	Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu		
	120	125	130
	135		

5 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 10 155 160 165 170
 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 15 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 20 205 210 215 220
 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 25 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 30 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 35 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Ser Leu Arg Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 40 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 45 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 50 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg

5	375	380	385	390
	Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu			
	395	400	405	
10	Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val			
	410	415	420	425
	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly			
15	430	435	440	
	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp			
	445	450	455	
20	Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met			
	460	465	470	475
	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg			
25	480	485	490	
	Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg			
	495	500	505	510
30	Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp			
	515	520	525	
	Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr			
35	530	535	540	
	Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro			
	545	550	555	560
40	Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp			
	565	570	575	
	Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro			
45	580	585	590	595
	Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro			
	600	605	610	
50	Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr			
	615	620	625	

5 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 10 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 15 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 20 700 705 710
 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 25 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
 30 750 755 760 765
 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
 770 775
 35

13. The replicable recombinant DNA as claimed in claim 8, which has a base sequence selected from the group consisting of those as shown in SEQ ID NO:10 and 11:

40
 SEQ ID NO:10:
 45 CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTA AAGCTCCCGT CGGATGAATA 60
 CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT 120
 GCAGGCTGGC GGCAAACCTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCACAG 180
 50 CGCCCCGGAG GAGGAACCCGG ACCACTCGGT GGCCGCCCTCC CTCGCAGCGC TGACCCAGAC 240
 TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCCACCGTT CCGGAGCCGA GGAAGACCAA 300
 GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA 360
 55 GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC 420

5 GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA 480
 CGAGGCAGCG GCGAAGCCCC CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC 540
 AGGCAAGCAG GGCAGGGACGG GCTC 564
 10 ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC 612
 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
 1 5 10 15
 15 ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG 660
 Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
 20 25 30
 20 GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC 708
 Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
 35 40 45
 25 GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
 Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
 50 55 60
 30 GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
 65 70 75 80
 35 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 40 TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
 Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 45 GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
 Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 50 GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG 996
 Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln

5	130	135	140
	CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG 1044		
	Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro		
10	145	150	155
	CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC 1092		
	Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His		
15	165	170	175
	GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA 1140		
	Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu		
20	180	185	190
	CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG 1188		
	Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg		
25	195	200	205
	GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC 1236		
	Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg		
30	210	215	220
	TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC 1284		
	Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp		
35	225	230	235
	240		
	GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC 1332		
	Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr		
40	245	250	255
	GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG 1380		
	Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln		
45	260	265	270
	TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC 1428		
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu		
50	275	280	285
	GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG 1476		

5 Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
 290 295 300
 GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG 1524
 10 Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
 305 310 315 320
 GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC 1572
 15 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 325 330 335
 TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT 1620
 20 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
 340 345 350
 CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC 1668
 25 Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716
 30 Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
 370 375 380
 GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764
 35 Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
 385 390 395 400
 CAG CTG CTG CAG CCG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812
 40 Gln Leu Leu Gln Pro Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
 405 410 415
 AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860
 45 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
 50 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445

5 GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
 Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
 450 455 460
 10 ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
 Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 15 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 20 ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
 Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
 500 505 510
 25 ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
 Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
 515 520 525
 30 GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 35 GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
 545 550 555 560
 40 CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
 Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
 565 570 575
 45 TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG CTG GGC CTC 2340
 Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
 580 585 590
 50 CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG 2388
 Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln

5	595	600	605
	CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG 2436		
	Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp		
10	610	615	620
	GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC 2484		
	Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala		
15	625	630	635
	GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC 2532		
	Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp		
20	645	650	655
	TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG 2580		
	Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu		
25	660	665	670
	CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628		
	Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val		
30	675	680	685
	CAT GCC AGG GGC CCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676		
	His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly		
35	690	695	700
	GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724		
	Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu		
40	705	710	715
	720		
	CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772		
	Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met		
45	725	730	735
	ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820		
	Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu		
50	740	745	750
	TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868		

Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr

5 755

760

765

GGA GGC AAG TCA

Gly Gly Lys Ser

10 770

TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGGCGCTTC GATATC 2936

15

20

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SEQ ID NO:11

GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTTGGTG 60

GGCATGTTCC TCAAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120

10 GACGTGAAC TCCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180

CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240

15 TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTTGTGCTT 300

CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360

CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCCTGCCGT TCCCGAGCCG 420

20 GCCAAGACGA AGAACGCCGGC CGCTGACCCCG GTTGCTGAAC CGGCCGACCC GCCGGTTGCT 480

GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCCGAACCG GGCTGCGGAG 540

CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600

25 GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660

CCCGCTGGGG AGGACGC 677

ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725

30 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe

1 5 10 15

ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773

35 Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly

20 25 30

GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC 821

40 Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser

35 40 45

45

50

55

5 GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
 Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
 50 55 60
 10 GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
 65 70 75 80
 15 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 20 ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
 Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 25 CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
 Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 30 GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
 Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 130 135 140
 35 CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
 Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 145 150 155 160
 40 CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
 Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
 165 170 175
 45 GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
 Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 180 185 190
 50 CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg

5	195	200	205	
	GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC 1349			
	Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg			
10	210	215	220	
	TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC 1397			
	Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp			
15	225	230	235	240
	GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC 1445			
	Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr			
20	245	250	255	260
	GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG 1493			
	Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln			
25	260	265	270	
	CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC 1541			
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu			
30	275	280	285	
	GCC GAC GTC GAC CCG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG 1589			
	Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu			
35	290	295	300	
	GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG 1637			
	Asp Arg Leu Asp Ala Ser Leu Arg Gly Glu Pro Ala Asp Tyr Gln			
40	305	310	315	320
	GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC 1685			
	Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His			
45	325	330	335	
	TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT 1733			
	Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val			
50	340	345	350	
	TCA ATC GAC GCC GGA GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC 1781			

5 Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829
 10 Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
 370 375 380
 GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC 1877
 15 Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
 385 390 395 400
 CAG GCT CTG CAG CCG CTG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925
 20 Gln Ala Leu Gln Pro Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
 405 410 415
 CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973
 25 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
 30 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
 35 Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
 450 455 460
 CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
 40 Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
 45 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
 50 Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
 500 505 510

5 GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
 Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
 515 520 525
 10 GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 15 GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
 545 550 555 560
 20 CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
 Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
 565 570 575
 25 TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC 2453
 Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
 580 585 590
 30 CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC AAG CTC GTG CAG 2501
 Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 595 600 605
 35 CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG 2549
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 610 615 620
 40 GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC 2597
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
 625 630 635 640
 45 GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG 2645
 Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
 645 650 655
 50 TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG 2693
 Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu

	660	665	670	
5	CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC			2741
	Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val			
10	675	680	685	
	CTG GCC AGC GGG CCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC			2789
	Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly			
15	690	695	700	
	ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC			2837
	Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr			
20	705	710	715	720
	GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC			2885
	Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn			
25	725	730	735	
	ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA			2933
	Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala			
30	740	745	750	
	GTG AAG ATC GCC GAC ATC TTC CCG TCG TTC CCC GTT GCG CTG CTG GTG			2981
	Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val			
35	755	760	765	
	CCG CAG ACA GGA GGA GAG TCA			3002
	Pro Gln Thr Gly Gly Glu Ser			
40	770	775		
	TGACGGCACAC CTACCCGCGG GAAGCCGCGA AACCCGTCCT GGGCCCCGCA CGCTACGACG			3062
	TCTGGGCGCC C			3073
45				

- 50 14. The replicable recombinant DNA as claimed in claim 8, wherein said DNA is derived from a microorganism selected from the group consisting of those of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curtobacterium*, *Mycobacterium* and *Terrabacter*.
- 55 15. The recombinant DNA as claimed in claim 8, wherein said self-replicable vector is a plasmid vector Blue-script II SK(+).
16. A transformant obtainable by introducing into a suitable host a recombinant DNA containing the DNA of claim 1 and a self-replicable vector.

17. The transformant as claimed in claim 16, wherein said DNA encodes an enzyme having the following physicochemical properties:

(1) Molecular weight

5 About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and

(2) Isoelectric point (pI)

About 3.6-4.6 on isoelectrophoresis.

18. The transformant as claimed in claim 16, wherein said DNA encodes an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

15 **SEQ ID NO:2**

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

1 5 10 15

20 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp

20 25 30

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly

25 35 40 45 50

Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu

55 60 65

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5 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 10 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 15 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 20 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 25 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 30 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 35 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 40 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 45 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 50 290 295 300 305
 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile

5	310	315	320	
	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu			
	325	330	335	340
10	Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala			
	345	350	355	
	Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr			
15	360	365	370	
	Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg			
	375	380	385	390
20	Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu			
	395	400	405	
	Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val			
25	410	415	420	425
	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly			
	430	435	440	
30	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu			
	445	450	455	
	Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met			
35	460	465	470	475
	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg			
	480	485	490	
40	Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg			
	495	500	505	510
	Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp			
45	515	520	525	
	Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr			
	530	535	540	
50	Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro			
	545	550	555	560

5 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 10 580 585 590 595
 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 15 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 20 630 635 640 645
 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 25 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 30 685 690 695
 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 35 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 40 735 740 745
 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 45 Pro Ala Thr Gly Gly Lys Ser
 770
 50

55 SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr

5	1	5	10	15
	Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp			
	20	25	30	
10	Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly			
	35	40	45	50
	Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Pro Glu			
15	55	60	65	
	Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu			
	70	75	80	85
20	Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro			
	90	95	100	
	Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala			
25	105	110	115	
	Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu			
	120	125	130	135
30	Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg			
	140	145	150	
	Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp			
35	155	160	165	170
	Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg			
	175	180	185	
40	Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu			
	190	195	200	
	Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu			
45	205	210	215	220
	Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His			
	225	230	235	
50	Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val			
	240	245	250	255
55				

5 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 10 275 280 285
 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 15 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 20 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 25 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 30 375 380 385 390
 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 35 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 40 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 45 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg

5 495 500 505 510
 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 10 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 15 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 20 545 550 555 560
 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 25 565 570 575
 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 30 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 35 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 40 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 45 630 635 640 645
 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 50 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 55 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 60 685 690 695
 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 65 700 705 710
 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 70 715 720 725 730
 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 75 735 740 745

Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

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5 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

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- 10 19. The transformant as claimed in claim 16, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequences to these base sequences:

15

SEQ ID NO:1

20 ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTTGAT 60
 GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTGCC 120
 ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180
 25 GACCCGGAGC GCGGCGGCC CGCCGGGTGT CCAAGGCGGC CCGCGGTGCC 240
 GGCAATGGCG TGCTGATCGA CATCGTGCCG AACACACGTGG GCGTGGCGTC GCGGCCGCAG 300
 AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGCGGGT CGCCCTACGC CGTGGCGTTC 360
 30 GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420
 GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCC 480
 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCGCAGG ACGTCCACGG CCGGCAGCAC 540
 35 TACGAACTCA TCGGCTGGCG GCGCGCCGAC AATGAACTGA ACTACCGCCG GTTCTTCGCG 600
 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCA 660
 GAGGTGGTGC GCTGGTTCCG TGCAGGGCTC GCCGACAGGG TGCGGATCGA CCACCCGGAC 720
 40 GGCCTGGCCG ATCCCGAGGG GTATTGAAG CGGCTCCGTG AGGTCAACCGG GGGCGCGTAC 780
 CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGGCAA 840
 GGCACCAACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCGGGGA 900
 45 CAGGTGCCGC TGGACCGTCT GGACGGCACGG CTGCGCGGCC GTGCGCCGGC CGACTACGAG 960
 GACATGATCC GCGGGACCAA GCGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
 CGCCTTGCCA GGCTGGTGCC CGAGCAGACC GGAATTCCCG GGGAGGCGGC CGCGGATGCG 1080
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5 ATCGCGGAGA TCATCGCGGC CTTCCCGGTACCGGTCTTACCTCCGA GGGCGCGGAG 1140
 ATCCTGAAGG AGGCCTGCGA CCTCGCCGCG CGGAGGCGTC CGGAACGTGGG CCAGACCGTC 1200
 CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
 10 ACCTCGGGAA TGGTCATGGC CAAAGGCGTG GAGGACACCG CGTTCTTCG CTACAACCGG 1320
 CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
 TTTCACGTCC GGATGGCCCG CCGGCAGGCC GAACTCCCGC TCTCCATGAC CACCGTGAGC 1440
 15 ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
 GCGCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCGGACGGC 1560
 CCGCTCTCCA CGCTGCTCTG GCAGGCGATT GCAGGGCAT GGCCGGCCAG CGGGAACGC 1620
 20 CTTCAGTCCT ACGCCCTGAA AGCGGCGCGC GAAGCCGGGA ACTCGACCAAG CTGGACCGAT 1680
 CCGGACCCGG CATTGAGGA GGCACCTTCC GCCGTCGTCG ACTCCGCCTT CGACAATCCG 1740
 GAGGTGCGTG CGGAACTTGA GGCCTGGTG GGCCTCCTTG CGCCGCACGG TGCGTCCAAC 1800
 25 TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGCG TTCCGGACGT GTACCAGGGC 1860
 ACCGAGTTCT GGGACAGGTC GCTGACCGAT CCGGACAACC GGCGCCCCCTT CAGCTCGCC 1920
 GAACGGATTA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
 30 GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCGGC TGCGGCGGAA CGGGCCCGAG 2040
 CTCTTCACCG GCTACCGCCC CGTGATGCC AGGGGGCCCG CCGCCGGGCA CCTGGTGGCG 2100
 TTCGACCGCG GCGCCGGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
 35 CAGTCGGCG GCTGGCGGGGA CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAACGT 2220
 ACCGGCTCCA CTTTCGGGCC GGGACCGGGCG GCGCTGTCAG AAGTCTTCCG GGCCTACCCG 2280
 GTGGCCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316
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SEQ ID NO:3

5 ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTAC ACTCTTCGAC 60
CGGGCCAAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
GTCCTGACTG CGGAGCAGGG CTCCGACAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
10 GACCCCGAAC GCGGCGGGCC GGAGGGCCTC GCGGCGGTTT CCAAGGCGGC CCGCGCCGCG 240
GGCATGGGCG TGCTGATCGA CATCGTGCCC AACCACGTGG GCGTCGCGAC GCCGGCCGAG 300
AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGGCGTTC 360

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5 GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
 GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGCGGT ACTACGACCA CCGATTCCCG 480
 CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGCGGG ATGTCCACGC CGGGCAGCAC 540
 10 TACGAGCTCA TCGGCTGGCG CCGCGCGGAC AACGAGCTGA ACTACCGCCG CTGGCTGGCG 600
 GTGAACACGC TCGCCGGCGT CCGCGTGGAA ATCCCCGCGC TCTTCGACGA GGCACACCAAG 660
 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCAGGACGGCC TGCGGATCGA CCACCCGGAC 720
 15 GGCCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGGGCCTTAC 780
 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CCGCCAGCTT CGAGTGTGAA 840
 GGCACACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGGCGGC 900
 20 CAGGAACCGC TGGACCGGCT TGACCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAAG 960
 GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
 CGGCTGGCCC GGCTGGTTCC GGGCGACGCC AACGTTCAA TCGACGCCGG AGCCGACGCT 1080
 25 CTCGCCGAAA TCATCGCCGC CTTCCCGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
 GTCTGAAGG AGGCGTGCAG GCTTGCCGCG CGTAGGCCGGC CGGAACCTCGA CCAGGCCATC 1200
 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGGCCGGCG CTTCCAGCAG 1260
 30 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCGGACGAG 1380
 TTCCACGCCG GGCTGGCACG CGGGCAGGCC GAGCTCCGC TGTCCATGAC GACGCTGAGC 1440
 35 ACGCACGACA CCAAGGCCAG CGAGGACACCC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
 GCGGGTGACT GGGAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCGCCT GCGGACGGC 1560
 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCGGGCGCCT GGGCCGCCAG CGGGAACGC 1620
 40 CTGCAGTACT ACGCGCTGAA GGCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
 CGGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCGCGGTGCG ACGCCGTGTT CGACAATCCC 1740
 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTCGAAC 1800
 45 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGCGC TCCCGGACGT CTACCAGGGC 1860
 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CGGGACAACC GCGGGCCGTT CAGCTCGAC 1920
 GACCGCCGCG CGCGCGTGGA GCAGCTGGAT GCGGGCGACC TTCCCGCGTC ATTTACCGAT 1980
 50 GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCCGGC TGCGCCGGGA CGTCCGGAG 2040
 CTGTTCACGG GGTACCGGCC GGTCCCTGGCC AGCGGGCCCCG CGGCCGGGCA CCTGCTCGCG 2100

TTCGACCGCG GCACCGCGGC GGCGCCGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
 5 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTG AACTAACAC CGCCATGAAA 2220
 GACGAACCTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATCTTCCGG 2280
 TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325

- 10 20. The transformant as claimed in claim 19, wherein one or more bases in SEQ ID NOS:1 and 3 are replaced with other bases by means of degeneracy of genetic code without altering their corresponding amino acid sequences as shown in the following SEQ ID NOS:2 and 4:

15

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
 20 1 5 10 15
 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 25 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 35 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 30 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 40 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 45 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 50 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 55 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 60 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 65 155 160 165 170

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5 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 10 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 15 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 20 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 25 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 30 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 35 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 40 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 290 295 300 305
 45 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 310 315 320
 50 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 55 Ala Asp Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 345 350 355
 60 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 360 365 370
 65 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390
 70 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 395 400 405
 75 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val

5 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 10 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 15 445 450 455
 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 20 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 25 480 485 490 495
 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 30 500 505 510
 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 35 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 40 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 45 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 50 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 55 580 585 590 595
 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 60 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 65 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 70 630 635 640 645
 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 75 650 655 660

Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
5 665 670 675 680
Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
685 690 695
10 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
700 705 710
Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
15 715 720 725 730
Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
735 740 745
20 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
750 755 760 765
Pro Ala Thr Gly Gly Lys Ser
25 770

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SEQ ID NO:4

5 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
1 5 10 15
Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
10 20 25 30
Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
15 35 40 45 50
Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
55 60 65
Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
20 70 75 80 85
Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
25 90 95 100
Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala

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5	105	110	115
	Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu		
	120	125	130
10	Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg		
	140	145	150
	Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp		
15	155	160	165
	Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg		
	175	180	185
20	Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu		
	190	195	200
	Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu		
25	205	210	215
	Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His		
	225	230	235
30	Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val		
	240	245	250
	Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln		
35	260	265	270
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala		
	275	280	285
40	Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg		
	290	295	300
	Leu Asp Ala Ser Leu Arg Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile		
45	310	315	320
	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu		
50	325	330	335
	Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly		
	345	350	355

5 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 10 375 380 385 390
 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 15 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 20 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 25 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 30 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 35 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 40 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 45 545 550 555 560
 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 50 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro

	600	605	610
5	Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr		
	615	620	625
	Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu		
10	630	635	640
	Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr		
	650	655	660
15	Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu		
	665	670	675
20	Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His		
	685	690	695
	Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu		
25	700	705	710
	Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr		
	715	720	725
30	Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe		
	735	740	745
	Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala		
35	750	755	760
	Leu Leu Val Pro Gln Thr Gly Gly Glu Ser		
	770	775	
40			

21. The transformant as claimed in claim 16, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:10 and 11:

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SEQ ID NO:10:

CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTTA AAGCTCCCGT CGGATGAATA	60
50 CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCCGT	120
GCAGGCTGGC GGCAAACCTCA CCCTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCACAG	180
55 CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCTCC CTCGCAGCGC TGACGCAGAC	240

5 TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300
 GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GC GGCGCCGA AGCCGGAAGA 360
 10 GAAGGCCTCC GACGAGGC GGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGC GGCGGC 420
 GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GGCGGCGAAG CCGGAAGAGG CTGCTTCCGA 480
 CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC 540
 15 AGGCAAGCAG GGC GGGACGG GCTC 564
 ATG AGG ACA CCC GCC TCG ACC TAC CGG CTG CAG ATC AGG CGG GGT TTC 612
 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
 20 1 5 10 15
 ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG 660
 Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
 25 20 25 30
 GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC 708
 Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
 30 35 40 45
 GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
 Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
 35 50 55 60
 GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
 40 65 70 75 80
 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 45 85 90 95
 TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
 Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 50 100 105 110
 GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
 Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly

5	115	120	125
	GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG 996		
	Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln		
10	130	135	140
	CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG 1044		
	Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro		
15	145	150	155
	CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC 1092		
	Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His		
20	165	170	175
	GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA 1140		
	Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu		
25	180	185	190
	CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG 1188		
	Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg		
30	195	200	205
	GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC 1236		
	Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg		
35	210	215	220
	TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC 1284		
	Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp		
40	225	230	235
	240		
	GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC 1332		
	Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr		
45	245	250	255
	GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GGC GAA CAG 1380		
	Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln		
50	260	265	270
	TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC 1428		

5

Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu
 275 280 285
 GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG 1476
 10 Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu
 290 295 300
 GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG 1524
 15 Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu
 305 310 315 320
 GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC 1572
 20 Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His
 325 330 335
 TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT 1620
 25 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile
 340 345 350
 CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC 1668
 30 Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716
 35 Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
 370 375 380
 GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764
 40 Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
 385 390 395 400
 CAG CTG CTG CAG CCG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812
 45 Gln Leu Leu Gln Pro Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
 405 410 415
 AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860
 50 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430

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5 ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 10 GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
 Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
 450 455 460
 15 ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
 Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 20 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 25 ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
 Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
 500 505 510
 30 ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
 Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
 515 520 525
 35 GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 40 GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
 545 550 555 560
 45 CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
 Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
 565 570 575
 50 TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC 2340
 Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu

	580	585	590	
5	CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG	2388		
	Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln			
10	595	600	605	
	CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG	2436		
	Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp			
15	610	615	620	
	GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC	2484		
	Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala			
20	625	630	635	640
	GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC	2532		
	Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp			
25	645	650	655	
	TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG	2580		
	Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu			
30	660	665	670	
	CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG	2628		
	Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val			
35	675	680	685	
	CAT GCC AGG GGC CCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC	2676		
	His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly			
40	690	695	700	
	GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA	2724		
	Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu			
45	705	710	715	720
	CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG	2772		
	Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met			
50	725	730	735	
	ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG	2820		

Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu
 740 745 750
 5 TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG TTG GTC CCC GCG ACA 2868
 Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr
 755 760 765
 10 GGA GGC AAG TCA 2880
 Gly Gly Lys Ser
 770
 15 TGACCGAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGCGCTTC GATATC 2936
 20

25 SEQ ID NO:11
 GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA GCGGCTTCGG CCGTCGGTG 60
 GGCAATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCGGCCG CCGCATCACG 120
 30 GACGTGAAC TCCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180
 CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CCGCCGGTGA AGGGGCCGAC 240
 TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCCG CCAAGTCGCT GGTTGTGCTT 300
 35 CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
 CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCTGCCGT TCCCAGGCCG 420
 GCCAAGACGA AGAAGCCGGC CGCTGACCCG GTTGCTGAAC CGGCGACCC GCCGGTTGCT 480
 40 GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACCG GGCTGCAGGAG 540
 CCTGCGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
 GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660
 45 CCCGCTGGGG AGGACGC 677
 ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725
 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe
 50 1 5 10 15
 ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773
 Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
 55 20 25 30

5 GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GCC TCC 821
 Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
 35 40 45
 10 GAC CAC GGG TAC GAC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
 Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
 50 55 60
 15 GGC GGG CCG GAG GGC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
 65 70 75 80
 20 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 25 ACG CCG GCG CAG AAC CCC TGG TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
 Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110
 30 CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
 Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 35 GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
 Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 130 135 140
 40 CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
 Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 145 150 155 160
 45 CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
 Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
 165 170 175
 50 GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
 Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu

	180	185	190	
5	CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC			1301
10	Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg			
	195	200	205	
15	GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC			1349
	Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg			
	210	215	220	
20	TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC			1397
	Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp			
	225	230	235	240
25	GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC			1445
	Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr			
	245	250	255	
30	GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG			1493
	Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln			
	260	265	270	
35	CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GGC TAC GAC GCC CTC			1541
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu			
	275	280	285	
40	GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG			1589
	Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu			
	290	295	300	
45	GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG			1637
	Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln			
	305	310	315	320
50	GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC			1685
	Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His			
	325	330	335	
	TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT			1733

5 Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val
 340 345 350
 TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC 1781
 10 Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829
 15 Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu
 370 375 380
 GCG TGC GAG CTT GCC GCG CGT AGG CCG CCG GAA CTC GAC CAG GCC ATC 1877
 20 Ala Cys Glu Leu Ala Ala Arg Arg Arg Pro Glu Leu Asp Gln Ala Ile
 385 390 395 400
 CAG GCT CTG CAG CCG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925
 25 Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg
 405 410 415
 CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973
 30 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
 35 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
 40 Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
 450 455 460
 CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
 45 Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
 50 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495

5 ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
 Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
 500 505 510
 10 GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
 Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
 515 520 525
 15 GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 20 GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
 545 550 555 560
 25 CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
 Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
 565 570 575
 30 TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC 2453
 Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
 580 585 590
 35 CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GCC AAG CTC GTG CAG 2501
 Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 595 600 605
 40 CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG 2549
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 610 615 620
 45 GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC 2597
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
 625 630 635 640
 50 GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG 2645
 Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala

5	645	650	655
	TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG	2693	
	Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu		
10	660	665	670
	CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC	2741	
	Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val		
15	675	680	685
	CTG GCC AGC GGG CCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC	2789	
	Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly		
20	690	695	700
	ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC	2837	
	Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr		
25	705	710	715
	GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC	2885	
	Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn		
30	725	730	735
	ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA	2933	
	Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala		
35	740	745	750
	GTG AAG ATC GCC GAC ATC TTC CCG TCG TTC CCC GTT GCG CTG CTG GTG	2981	
	Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val		
40	755	760	765
	CCG CAG ACA GGA GGA GAG TCA		3002
45	Pro Gln Thr Gly Gly Glu Ser		
	770	775	
	TGACGGCACAC CTACCCGGCGG GAAGCCGCGA AACCCGTCCCT GGGCCCCGCA CGCTACGACG	3062	
50	TCTGGGGGCC C		3073

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22. The transformant as claimed in claim 16, wherein said DNA is derived from a microorganism selected from the group consisting of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curtobacterium*, *Mycobacterium* and *Terrabacter*.

23. The transformant as claimed in claim 16, wherein said self-replicable vector is a plasmid vector Bluescript II SK(+).
- 5 24. The transformant as claimed in claim 16, wherein said host is a microorganism of the species *Escherichia coli*.
25. A recombinant enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher.
- 10 26. The recombinant enzyme as claimed in claim 25, which has the following physicochemical properties:
(1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
(2) Isoelectric point (pi)
About 3.6-4.6 on isoelectrophoresis.
- 15 27. The recombinant enzyme as claimed in claim 25, which has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOS:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:
- 20

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

25 1 5 10 15

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp

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 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 10 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 15 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 20 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 25 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 30 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 35 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 40 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 45 155 160 165 170
 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 50 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 55 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 60 205 210 215 220
 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 65 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 70 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 75 260 265 270

5 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285

10 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg
 290 295 300 305

15 Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile
 310 315 320

20 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340

25 Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala
 345 350 355

30 Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr
 360 365 370

35 Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg
 375 380 385 390

40 Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu
 395 400 405

45 Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser-Gly Met Val
 410 415 420 425

50 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440

55 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu
 445 450 455

60 Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475

65 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490

70 Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg
 495 500 505 510

75 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp

5 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 10 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 15 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 20 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 25 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 30 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 35 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 40 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 45 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 50 735 740 745
 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765

Pro Ala Thr Gly Gly Lys Ser

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SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr

1 5 10 15

Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
10 20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
15 35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
20 55 60 65

Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
25 70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
25 90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
30 105 110 115

Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
35 140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
40 155 160 165 170

Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
45 190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
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	205	210	215	220
	Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His			
10		225	230	235
	Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val			
	240	245	250	255
15	Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln			
	260	265	270	
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala			
20	275	280	285	
	Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg			
	290	295	300	305
25	Leu Asp Ala Ser Leu Arg Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile			
	310	315	320	
	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu			
30	325	330	335	340
	Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly			
	345	350	355	
35	Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr			
	360	365	370	
	Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg			
40	375	380	385	390
	Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu			
	395	400	405	
45	Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val			
	410	415	420	425
	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly			
50	430	435	440	
	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp			
	445	450	455	

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5 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 10 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 15 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 20 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 545 550 555 560
 25 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 30 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 35 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 40 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 630 635 640 645
 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 45 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asp Arg Pro Glu
 665 670 675 680
 50 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu

	700	705	710	
5	Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr			
	715	720	725	730
	Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe			
10	735	740	745	
	Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala			
	750	755	760	765
15	Leu Leu Val Pro Gln Thr Gly Gly Glu Ser			
	770	775		

- 20 28. A process for producing a recombinant enzyme, which comprises culturing a transformant capable of forming the recombinant enzyme of claim 25, and collecting the recombinant enzyme from the resultant culture.
- 25 29. The process as claimed in claim 28, wherein said recombinant enzyme has the following physicochemical properties:
- (1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
 - (2) Isoelectric point (pi)
About 3.6-4.6 on isoelectrophoresis.
- 30 30. The process of as claimed in claim 28, wherein said recombinant enzyme has an amino acid sequence selected from the group consisting of those as shown in SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

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SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

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5 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 10 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 15 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 20 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 25 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 30 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 35 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 40 190 195 200
 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 45 205 210 215 220
 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 50 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

5	260	265	270
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala		
	275	280	285
10	Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg		
	290	295	300
	Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile		
15	310	315	320
	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu		
	325	330	335
20	340	345	350
	Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala		
	355	360	365
	Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr		
25	370	375	380
	Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg		
	390	395	400
30	405	410	415
	Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu		
	420	425	430
	Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val		
35	435	440	445
	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly		
	455	460	465
40	470	475	480
	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu		
	485	490	495
45	500	505	510
	Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met		
	515	520	525
	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg		
50	530	535	540
	Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg		
	545	550	555
55	560	565	570

5 Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp
 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 10 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 15 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 20 580 585 590 595
 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 25 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 30 630 635 640 645
 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 35 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 40 685 690 695
 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 45 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 50 735 740 745
 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val

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Pro Ala Thr Gly Gly Lys Ser

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SEQ ID NO:4

15 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 35 40 45 50
 25 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 30 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 90 95 100
 35 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 40 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 140 145 150
 45 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 155 160 165 170
 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 50 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 55 190 195 200

5 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 10 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 15 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 20 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 25 290 295 300 305
 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 310 315 320
 30 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 35 345 350 355
 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 360 365 370
 40 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 45 395 400 405
 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 50 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp

5	445	450	455
	Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met		
460	465	470	475
10	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg		
	480	485	490
	Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg		
15	495	500	505
	Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp		
	515	520	525
20	Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr		
	530	535	540
	Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro		
25	545	550	555
	Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp		
	565	570	575
30	Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro		
	580	585	590
	Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro		
35	600	605	610
	Gly Val Pro Asp Val Tyr Gin Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr		
	615	620	625
40	Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu		
	630	635	640
	645		
45	Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr		
	650	655	660
	Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Asp Arg Pro Glu		
50	665	670	675
	680		
	Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His		
	685	690	695

Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 5 700 705 710
 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 10 Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
 15 750 755 760 765
 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
 770 775

- 20
31. The process as claimed in claim 28, wherein said transformant is obtained by introducing into a suitable host a recombinant DNA containing a self-replicable vector and a DNA encoding an enzyme which forms a non-reducing saccharide having trehalose structure as an end unit from a reducing amyloseous saccharide having a degree of glucose polymerization of 3 or higher.
 - 25
 32. The process as claimed in claim 28, wherein said DNA has a base sequence selected from the group consisting of those as shown in SEQ ID NOs:1 and 3 that initiate from the 5'-terminus, homologous base sequences to the base sequences, and complementary base sequence to these base sequences:
- 30

SEQ ID NO:1

35 ATGAGGACAC CCGCCTCGAC CTACCGGCTG CAGATCAGGC GGGGTTTCAC GCTGTGGAT 60
 GCCGCCGAGA CCGTGCCCTA CCTGAAGTCA CTCGGGGTGG ACTGGATCTA CCTGTGCC 120
 ATCCTGAAGG CAGAGAGCGG CTCCGACCAC GGCTATGACG TCACCGATCC CGCCGTAGTG 180
 40 GACCCGGAGC GCGGCGGCC TGAAGGGCTG GCCGCGGTGT CCAAGGCGGC CCGCGGTGCC 240
 GGCATGGCG TGCTGATCGA CATCGTGCCG AACCACGTGG GCCTGGCGTC GCCGCCAG 300
 AACCCGTGGT GGTGGTCGCT GCTCAAGGAA GGGCGGGGT CGCCCTACGC CGTGGCGTTC 360

45

50

55

5 GACGTCGACT GGGACCTGGC GGGGGGCCGC ATCCGGATCC CCGTCCTGGG CAGCGACGAC 420
 GATCTGGACC AGCTCGAAAT CAAGGACGGC GAGCTGCGGT ACTACGACCA CCGCTTCCCG 480
 CTGGCCGAGG GCAGCTACCG GGACGGCGAC TCCCCCAGG ACGTCCACGG CGGGCAGCAC 540
 10 TACGAACCTCA TCGGCTGGCG GCGCGCCGAC AATGAACCTGA ACTACCGCCG GTTCTTCGCG 600
 GTGAACACGC TCGCCGGCAT CCGGGTGGAG GTGCCGCCGG TCTTCGATGA AGCGCACCAG 660
 GAGGTGGTGC GCTGGTCCG TGCGGGCTC GCCGACGGC TGCGGATCGA CCACCCGGAC 720
 15 GCCCTGGCCG ATCCCAGGG GTATTTGAAG CGGCTCCGTG AGGTACCCGG GGGCGCGTAC 780
 CTGCTCATCG AAAAGATCCT CGAGCCGGGC GAACAGTTGC CGGCCAGCTT CGAGTGCAGA 840
 GGCACCACCG GCTACGACGC CCTCGCGGAT GTCGACAGGG TCTTCGTGGA CCCGCCGGGA 900
 20 CAGGTGCCGC TGGACCGTCT GGACGCACGG CTGCGCCGG GTGCCGCCGG CGACTACGAG 960
 GACATGATCC GCGGGACCAA CGGCCGGATC ACCGACGGCA TCCTGCACTC CGAGATCCTG 1020
 CGCCTTGCCA GGCTGGTGC CGAGCAGACC GGAATTCCCG GGGAGGCCGG CGCGGATGCG 1080
 25 ATCGCGGAGA TCATCGCGC CTTCCCGGT TACCGGTCTT ATCTTCCCGA GGGCGCGGAG 1140
 ATCCTGAAGG AGGCCTGCGA CCTCGCCGG CGGAGGCCGT CGGAACTGGG CCAGACCGTC 1200
 CAGCTGCTGC AGCCGCTGCT GCTGGATACC GACCTCGAGA TTTCCCGCAG GTTCCAGCAG 1260
 30 ACCTCGGGAA TGGTCATGGC CAAAGGCCGTG GAGGACACCG CGTTCTTCCG CTACAACCGG 1320
 CTGGGAACGC TCACCGAGGT GGGCGCCGAC CCCACCGAGT TCTCGCTGGA ACCGGAGGAG 1380
 TTTCACGTCC GGATGGCCCG CCGGCAGGCC GAACTCCCGC TCTCCATGAC CACCGTGCAG 1440
 35 ACGCACGACA CCAAGCGCAG CGAGGACACC CGGGCCCGGA TCTCGGTGAT CGCCGAGGTC 1500
 GCCCCTGAAT GGGAAAAGGC CCTGGACAGG CTGAACACCC TCGCTCCGCT GCCGGACGGC 1560
 CCGCTCTCCA CGCTGCTCTG GCAGGCCATT GCGGGGGCAT GCCCGGCCAG CGGGAACGC 1620
 40 CTTCAGTCCT ACGCCCTGAA AGCGGCCGC GAAGCCGGGA ACTCGACCAAG CTGGACCGAT 1680
 CCGGACCCGG CATTGAGGA GCCACTTCC GCCGTGCTCG ACTCCGCCCT CGACAATCCG 1740
 GAGGTGCGTG CGGAACCTTGA GGCCTGGTG GGCCTCCCTG CGCCGCACGG TGCGTCCAAC 1800
 45 TCGCTCGCGG CAAAGCTTGT CCAGCTGACC ATGCCGGCG TTCCGGACGT GTACCAGGGC 1860
 ACCGA~~TTCT~~ GGGACAGGTC GCTGACCGAT CGGGACAACC GGCGCCCCCTT CAGCTTCGCC 1920
 50 GAACGGATTAA GGGCCTTGGA CCAGTTGGAC GCCGGCCACC GTCCGGACTC CTTCCAGGAC 1980
 GAGGCGGTCA AGCTGCTGGT CACCTCGAGG GCGCTGCCGG TGCGGCCGGAA CGGGCCCGAG 2040
 CTCTTACCG GCTACCGCCC CGTGCATGCC AGGGGCCCG CGCCGGGCA CCTGGTGGCG 2100

5 TTCGACCGCG GCGCCGGGG AGTGCTGGCG CTTGCCACCC GGCTCCCCTA CGGGCTGGAA 2160
 CAGTCGGCG GCTGGCGGA CACCGCCGTC GAGCTTGAAG CCGCCATGAC GGACGAAC TG 2220
 ACCGGCTCCA CTTCGGGCC GGGACCGCG GCGCTGTCAAG AAGTCTTCCG GCCCTACCCG 2280
 GTGGCCTTGT TGGTCCCCGC GACAGGAGGC AAGTCA 2316

10

15 SEQ ID NO:3
 ATGAGAACGC CAGTCTCCAC GTACAGGCTG CAGATCAGGA AGGGATTAC ACTCTCGAC 60
 GCGGCCAAAA CCGTTCCGTA CCTGCACTCG CTCGGCGTCG ACTGGGTCTA CCTTTCTCCG 120
 20 GTCCTGACTG CCGAGCAGGG CTCCGACCAC GGGTACGACG TCACCGATCC CTCCGCCGTC 180
 GACCCCGAAC GCGGCAGGGC GGAGGGCCTC GCGCGGTTT CCAAGGCGGC CGCGGCCGCG 240
 GGCATGGCG TGCTGATCGA CATCGTCCCC AACACGTGG GCGTCGCGAC GCGGGCGCAG 300
 25 AACCCCTGGT GGTGGTCGCT GCTCAAGGAG GGACGCCAGT CCCGTTACGC GGAGGCGTTC 360
 GACGTCGATT GGGACCTCGC CGGGGGACGC ATCCGGCTGC CGGTGCTCGG CAGCGACGAT 420
 GACCTCGACC AGCTCGAAAT CAGGGACGGG GAGCTGGGT ACTACGACCA CCGATTCCCG 480
 30 CTCGCCGAGG GAACCTACGC CGAAGGCGAC GCCCCGGGG ATGTCACCGC CGGGCAGCAC 540
 TACGAGCTCA TCGGCTGGCG CCGCGCGAC AACGAGCTGA ACTACCGCCG CTTTTTCGCG 600
 GTGAACACGC TCGCCGGCGT CGCGTGGAA ATCCCCGCCG TCTTCGACGA GGCACACCGAG 660
 35 GAGGTGGTGC GCTGGTTCCG CGAGGACCTT GCGGACGCC TGCGGATCGA CCACCCGGAC 720
 GGCCTCGCTG ACCCCGAGGG GTACCTGAAG CGACTCCGGG AAGTCACCGG CGCGCCTTAC 780
 CTGCTGATCG AAAAGATCCT GGAGCCGGGG GAGCAGCTGC CGGCCAGCTT CGAGTGTGAA 840
 40 GGCACACAG GCTACGACGC CCTCGCCGAC GTCGACCGGG TTCTCGTGGA CCCGCGCGC 900
 CAGGAACCGC TGGACCGGCT TGACCGTCC CTGCGTGGCG GCGAGCCCGC CGACTACCAG 960
 GACATGATCC GCGGAACCAA GCGCCGGATC ACCGACGGTA TCCTGCACTC GGAGATCCTG 1020
 45 CGGCTGGCCC GGCTGGTTCC GGGGACGCC AACGTTCAA TCGACGCCGG AGCCGACGCT 1080
 CTCGCCGAAA TCATCGCCGC CTTCCCGGTC TACCGCACCT ACCTGCCGGA GGGCGCCGAG 1140
 GTCCTGAAGG AGGCGTGCAG GCTTGCCGCG CGTAGGCGGC CGGAACTCGA CCAGGCCATC 1200
 50 CAGGCTCTGC AGCCGCTGCT GCTGGACACG GACCTCGAGC TTGCCCGGCG CTTCCAGCAG 1260
 ACCTCGGGCA TGGTCATGGC CAAGGGCGTG GAGGACACCG CGTTCTTCCG CTACAACCGC 1320
 CTGGGCACCC TCACGGAAGT GGGCGCCGAC CCCACCGAGT TCGCCGTGGA GCGGACGAG 1380

55

TTCCACGCC CGCTGGCACG CGGCAGGCC GAGCTCCGC TGTCCATGAC GACGCTGAGC 1440
 5 ACGCACGACA CCAAGCGCAG CGAGGACACC CGAGCAAGGA TTTCGGTCAT TTCCGAGGTT 1500
 GCGGGTGACT GGGAAAAGGC CTTGAACCGG CTGCGCGACC TGGCCCCGCT GCCGGACGGC 1560
 CCGCTGTCCG CGCTGCTCTG GCAGGCCATT GCCGGCCCT GGCCCGCCAG CCGGGAACGC 1620
 10 CTGCAGTACT ACGCGCTGAA GGCCGCGCGT GAAGCGGGGA ACTCGACCAA CTGGACCGAT 1680
 CGGGCCCCCG CGTTCGAGGA GAAGCTGAAG GCCGCGGTGCG ACGCCGTGTT CGACAATCCC 1740
 GCCGTGCAGG CCGAGGTGGA AGCCCTCGTC GAGCTCCTGG AGCCGTACGG AGCTTCGAAC 1800
 15 TCCCTCGCCG CCAAGCTCGT GCAGCTGACC ATGCCCGCG TCCCGGACGT CTACCAGGGC 1860
 ACGGAGTTCT GGGACCGGTC GCTGACGGAC CCGGACAACC GGCGGCCGTT CAGCTTCGAC 1920
 GACCGCCGCG CCGCGCTGGA GCAGCTGGAT GCCGGCGACC TTCCCGCGTC ATTACCGAT 1980
 20 GAGCGGACGA AGCTGCTAGT GACGTCGCGC GCGCTGCGC TGCGCCGGGA CCGTCCGGAG 2040
 CTGTTACCGG GGTACCGGCC GGTCCCTGGCC AGCGGGCCCG CCGCCGGGCA CCTGCTCGCG 2100
 TTCGACCGCG GCACCGCGGC GGCGCCGGGT GCATTGACCC TCGCCACGCG GCTTCCCTAC 2160
 25 GGGCTGGAAC AGTCGGGTGG ATGGCGGGAC ACCGCCGTG AACTTAACAC CGCCATGAAA 2220
 GACGAACGTGA CCGGTGCCGG CTTCGGACCG GGGGCAGTGA AGATCGCCGA CATTTCCGG 2280
 TCGTTCCCCG TTGCGCTGCT GGTGCCGCAG ACAGGAGGAG AGTCA 2325
 30

33. The process as claimed in claim 32, wherein said DNA has a base sequence selected from the group consisting of those as shown in SEQ.ID NOs:1 and 3 wherein one or more bases are replaced with other bases by means of degeneracy of genetic code without altering their corresponding amino acid sequences as shown in the following SEQ ID NOs:2 and 4:
 35

40 **SEQ ID NO:2**
 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr
 1 5 10 15
 45 Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp
 20 25 30
 Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly
 50 35 40 45 50

5 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 10 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100
 15 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 20 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 25 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 30 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 35 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 40 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 45 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 50 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg

5	290	295	300	305
	Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile			
	310	315	320	
10	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu			
	325	330	335	340
	Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala			
15	345	350	355	
	Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr			
	360	365	370	
20	Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg			
	375	380	385	390
	Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu			
25	395	400	405	
	Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val			
	410	415	420	425
30	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly			
	430	435	440	
	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu			
35	445	450	455	
	Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met			
	460	465	470	475
40	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg			
	480	485	490	
	Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg			
45	495	500	505	510
	Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp			
	515	520	525	
50	Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr			
	530	535	540	

5 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 10 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 15 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 20 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 25 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 30 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 35 Leu Val Ala Phe Asp Arg Gly Ala Gly Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 40 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 735 740 745
 45 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 50 Pro Ala Thr Gly Gly Lys Ser
 770

5 SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15

10 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30

Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 15 35 40 45 50

Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65

20 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85

Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 25 90 95 100

Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115

30 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135

Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 35 140 145 150

Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 155 160 165 170

40 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185

Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 45 190 195 200

Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220

50 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235

5 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 10 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 15 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 20 310 315 320
 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 25 Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 30 360 365 370
 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 35 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu Leu
 395 400 405
 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 40 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 45 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 50 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg
 55

5	480	485	490	
	Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg			
	495	500	505	510
10	Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp			
	515	520	525	
	Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr			
15	530	535	540	
	Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro			
	545	550	555	560
20	Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp			
	565	570	575	
	Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro			
25	580	585	590	595
	Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro			
	600	605	610	
30	Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr			
	615	620	625	
	Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu			
35	630	635	640	645
	Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr			
	650	655	660	
40	Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Asp Arg Pro Glu			
	665	670	675	680
	Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His			
45	685	690	695	
	Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu			
50	700	705	710	
	Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr			
	715	720	725	730

Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe
 735 740 745
 5 Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala
 750 755 760 765
 10 Leu Leu Val Pro Gln Thr Gly Gly Glu Ser
 770 775

34. The process as claimed in claim 28, wherein said DNA has a base sequence selected from the group consisting of those as shown in the following SEQ ID NOs:10 and 11:

20 SEQ ID NO:10:

CGTGCTCTAC TTCAACGCGC ACGACGGCGA CGTCGTGTT AAGCTCCGT CGGATGAATA 60
 CGCCCCGGCC TGGGACGTCA TCATCGACAC CGCCGGCGCG GGTGCCGATT CCGAACCGT 120
 25 GCAGGCTGGC GGCAAACTCA CCGTGGCAGC GAAATCGCTC GTGGTGCTCC GTGCCACAG 180
 CGCCCCGGAG GAGGAACCGG ACCACTCGGT GGCCGCCCTCC CTCCGAGCGC TGACGCAGAC 240
 TGCGACCGCC GAAACCGCGG CGCTCACCGC CCCCACCGTT CCGGAGCCGA GGAAGACCAA 300
 30 GAAGGCAGCG CCGAAGCCGG AAGAGGAGGC TCCCGACGAG GCGGCGCCGA AGCCGGAAGA 360
 GAAGGCTCCC GACGAGGCGG CGGCGAAGCC GGAAGAGGCT GCTTCCGACG AGGCGGCGGC 420
 GAAGCCGGAA GAGAAGGCTC CCGACGAGGC GCGGGCGAAG CCGGAAGAGG CTGCTTCCGA 480
 35 CGAGGCGGCG GCGAAGCCCG CGGGGAAGGC AGCGGCCAAA ACGGCCGGCA GGCGAGCGCC 540
 AGGCAAGCAG GGCAGGGACGG GCTC 564
 ATG AGG ACA CCC GCC TCG ACC TAC CCG CTG CAG ATC AGG CGG GGT TTC 612
 40 Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe
 1 5 10 15
 ACG CTG TTT GAT GCC GCC GAG ACC GTG CCC TAC CTG AAG TCA CTC GGG 660
 45 Thr Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly
 20 25 30
 GTG GAC TGG ATC TAC CTG TCG CCC ATC CTG AAG GCA GAG AGC GGC TCC 708
 50 Val Asp Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser
 35 40 45

5 GAC CAC GGC TAT GAC GTC ACC GAT CCC GCC GTA GTG GAC CCG GAG CGC 756
 Asp His Gly Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg
 50 55 60

10 GGC GGC CCT GAA GGG CTG GCC GCG GTG TCC AAG GCG GCC CGC GGT GCC 804
 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala
 65 70 75 80

15 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCG AAC CAC GTG GGC GTG GCG 852
 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95

20 TCG CCG CCG CAG AAC CCG TGG TGG TGG TCG CTG CTC AAG GAA GGG CGC 900
 Ser Pro Pro Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110

25 GGG TCG CCC TAC GCC GTG GCG TTC GAC GTC GAC TGG GAC CTG GCG GGG 948
 Gly Ser Pro Tyr Ala Val Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125

30 GGC CGC ATC CGG ATC CCC GTC CTG GGC AGC GAC GAC GAT CTG GAC CAG 996
 Gly Arg Ile Arg Ile Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 130 135 140

35 CTC GAA ATC AAG GAC GGC GAG CTG CGG TAC TAC GAC CAC CGC TTC CCG 1044
 Leu Glu Ile Lys Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 145 150 155 160

40 CTG GCC GAG GGC AGC TAC CGG GAC GGC GAC TCC CCG CAG GAC GTC CAC 1092
 Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp Ser Pro Gln Asp Val His
 165 170 175

45 GGC CGG CAG CAC TAC GAA CTC ATC GGC TGG CGG CGC GCC GAC AAT GAA 1140
 Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 180 185 190

50 CTG AAC TAC CGC CGG TTC TTC GCG GTG AAC ACG CTC GCC GGC ATC CGG 1188
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Ile Arg

5	195	200	205	
	GTG GAG GTG CCG CCG GTC TTC GAT GAA GCG CAC CAG GAG GTG GTG CGC 1236			
	Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu Val Val Arg			
10	210	215	220	
	TGG TTC CGT GCG GGG CTC GCC GAC GGG CTG CGG ATC GAC CAC CCG GAC 1284			
	Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp			
15	225	230	235	240
	GGC CTG GCC GAT CCC GAG GGG TAT TTG AAG CGG CTC CGT GAG GTC ACC 1332			
	Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr			
20	245	250	255	
	GGG GGC GCG TAC CTG CTC ATC GAA AAG ATC CTC GAG CCG GCC GAA CAG 1380			
	Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln			
25	260	265	270	
	TTG CCG GCC AGC TTC GAG TGC GAA GGC ACC ACC GGC TAC GAC GCC CTC 1428			
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu			
30	275	280	285	
	GCG GAT GTC GAC AGG GTC TTC GTG GAC CCG CGG GGA CAG GTG CCG CTG 1476			
	Ala Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu			
35	290	295	300	
	GAC CGT CTG GAC GCA CGG CTG CGC GGC GGT GCG CCG GCC GAC TAC GAG 1524			
	Asp Arg Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu			
40	305	310	315	320
	GAC ATG ATC CGC GGG ACC AAG CGC CGG ATC ACC GAC GGC ATC CTG CAC 1572			
	Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His			
45	325	330	335	
	TCC GAG ATC CTG CGC CTT GCC AGG CTG GTG CCC GAG CAG ACC GGA ATT 1620			
50	Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile			
	340	345	350	
	CCC GGG GAG GCG GCC GCG GAT GCG ATC GCG GAG ATC ATC GCG GCC TTC 1668			

5 Pro Gly Glu Ala Ala Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe
 355 360 365
 CCG GTC TAC CGG TCC TAT CTT CCC GAG GGC GCG GAG ATC CTG AAG GAG 1716
 10 Pro Val Tyr Arg Ser Tyr Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu
 370 375 380
 GCC TGC GAC CTC GCC GCG CGG AGG CGT CCG GAA CTG GGC CAG ACC GTC 1764
 15 Ala Cys Asp Leu Ala Ala Arg Arg Arg Pro Glu Leu Gly Gln Thr Val
 385 390 395 400
 CAG CTG CTG CAG CCG CTG CTG CTG GAT ACC GAC CTC GAG ATT TCC CGC 1812
 20 Gln Leu Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Ile Ser Arg
 405 410 415
 AGG TTC CAG CAG ACC TCG GGA ATG GTC ATG GCC AAA GGC GTG GAG GAC 1860
 25 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGG CTG GGA ACG CTC ACC GAG GTG GGC 1908
 30 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 GCC GAC CCC ACC GAG TTC TCG CTG GAA CCG GAG GAG TTT CAC GTC CGG 1956
 35 Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu Glu Phe His Val Arg
 450 455 460
 ATG GCC CGC CGG CAG GCC GAA CTC CCG CTC TCC ATG ACC ACC CTG AGC 2004
 40 Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGG GCC CGG ATC TCG GTG 2052
 45 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 ATC GCC GAG GTC GCG CCT GAA TGG GAA AAG GCC CTG GAC AGG CTG AAC 2100
 50 Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg Leu Asn
 500 505 510

5 ACC CTC GCT CCG CTG CCG GAC GGC CCG CTC TCC ACG CTG CTC TGG CAG 2148
 Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp Gln
 515 520 525
 10 GCG ATT GCG GGG GCA TGG CCG GCC AGC CGG GAA CGC CTT CAG TCC TAC 2196
 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr
 530 535 540
 15 GCC CTG AAA GCG GCG CGC GAA GCC GGG AAC TCG ACC AGC TGG ACC GAT 2244
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp
 545 550 555 560
 20 CCG GAC CCG GCA TTC GAG GAG GCA CTT TCC GCC GTC GTC GAC TCC GCC 2292
 Pro Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala
 565 570 575
 25 TTC GAC AAT CCG GAG GTG CGT GCG GAA CTT GAG GCC CTG GTG GGC CTC 2340
 Phe Asp Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu
 580 585 590
 30 CTT GCG CCG CAC GGT GCG TCC AAC TCG CTC GCG GCA AAG CTT GTC CAG 2388
 Leu Ala Pro His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 595 600 605
 35 CTG ACC ATG CCG GGC GTT CCG GAC GTG TAC CAG GGC ACC GAG TTC TGG 2436
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 610 615 620
 40 GAC AGG TCG CTG ACC GAT CCG GAC AAC CGG CGC CCC TTC AGC TTC GCC 2484
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala
 625 630 635 640
 45 GAA CGG ATT AGG GCC TTG GAC CAG TTG GAC GCC GGC CAC CGT CCG GAC 2532
 Glu Arg Ile Arg Ala Leu Asp Gln Leu Asp Ala Gly His Arg Pro Asp
 645 650 655
 50 TCC TTC CAG GAC GAG GCG GTC AAG CTG CTG GTC ACC TCG AGG GCG CTG 2580
 Ser Phe Gln Asp Glu Ala Val Lys Leu Leu Val Thr Ser Arg Ala Leu

5	660	665	670
	CGG CTG CGG CGG AAC CGG CCC GAG CTC TTC ACC GGC TAC CGC CCC GTG 2628		
	Arg Leu Arg Arg Asn Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val		
10	675	680	685
	CAT GCC AGG GGC CCC GCC GGG CAC CTG GTG GCG TTC GAC CGC GGC 2676		
	His Ala Arg Gly Pro Ala Ala Gly His Leu Val Ala Phe Asp Arg Gly		
15	690	695	700
	GCC GGG GGA GTG CTG GCG CTT GCC ACC CGG CTC CCC TAC GGG CTG GAA 2724		
	Ala Gly Gly Val Leu Ala Leu Ala Thr Arg Leu Pro Tyr Gly Leu Glu		
20	705	710	715
	CAG TCG GGC GGC TGG CGG GAC ACC GCC GTC GAG CTT GAA GCC GCC ATG 2772		
	Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Glu Ala Ala Met		
25	725	730	735
	ACG GAC GAA CTG ACC GGC TCC ACT TTC GGG CCG GGA CCG GCG GCG CTG 2820		
	Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly Pro Ala Ala Leu		
30	740	745	750
	TCA GAA GTC TTC CGG GCC TAC CCG GTG GCC TTG GTC CCC GCG ACA 2868		
	Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val Pro Ala Thr		
35	755	760	765
	GGA GGC AAG TCA 2880		
	Gly Gly Lys Ser		
40	770		
	TGACGCAGCC CAACGATGCG GCCAAGCCGG TGCAGGGAGC GGGCGCTTC GATATC 2936		

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SEQ ID NO:11

5 GATCCGGACG GCAACCTCAT GTCCCCGGAG GACTGGGACA CGGGCTTCGG CCGTTCCGTG 60
GGCATGTTCC TCAACGGCGA CGGCATCCAG GGCCACGATG ACCGCAGGCC CGGCATCACCG 120
GACGTGAAC TCCCTGCTGTA CTTCAACGCC CACGACGGCG ACGTCGAGTT CACGCTGCCG 180
10 CCGGACGAAT ACGCCCCGGC CTGGGACGTC ATCATCGACA CGGCCGGTGA AGGGGCCGAC 240

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5 TCCAAGCCCG CGGACGCCGG AACCATCCTG TCCGTTGCGG CCAAGTCGCT GGTTGTGCTT 300
 CGCGCCCACA GCGCACCGGA GGAGGAGCCT GACCATTCCG TGGCTGCTTC CCTGGCTGCA 360
 CTGACGCAGA CCGCCACCGC CGAGACGGCG GCGCTCACAG CTCCCTGCCGT TCCCGAGCCG 420
 10 GCCAAGACGA AGAACGCCGGC CGCTGACCCG GTTGCTGAAC CGGCGACCC GCCGGTTGCT 480
 GACCCGGCCG ACCCGGTTGC TGACCCGGTT GCTGACCCGG CGCCGGAACC GGCTGCGGAG 540
 CCTGCAGAAAT CCGCAGCGGA ACCTGGTGCG GAGCCTGCGA AGGACCCGGA GGAGCAGCCG 600
 15 GCGGAAAAGC CGGCGCGCAA GCCTGCGGCA AAGCGCGGCG GCCACCTGAG GGCGGTCAAG 660
 CCCGCTGGGG AGGACGC 677
 ATG AGA ACG CCA GTC TCC ACG TAC AGG CTG CAG ATC AGG AAG GGA TTC 725
 20 Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe
 1 5 10 15
 ACA CTC TTC GAC GCG GCC AAA ACC GTT CCG TAC CTG CAC TCG CTC GGC 773
 25 Thr Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly
 20 25 30
 GTC GAC TGG GTC TAC CTT TCT CCG GTC CTG ACT GCC GAG CAG GGC TCC 821
 30 Val Asp Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser
 35 40 45
 GAC CAC GGG TAC GAC GTC ACC GAT CCC TCC GCC GTC GAC CCC GAA CGC 869
 35 Asp His Gly Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg
 50 55 60
 GGC GGG CCG GAG GCC CTC GCG GCG GTT TCC AAG GCG GCC CGC GCC GCG 917
 40 Gly Gly Pro Glu Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala
 65 70 75 80
 GGC ATG GGC GTG CTG ATC GAC ATC GTG CCC AAC CAC GTG GGC GTC GCG 965
 45 Gly Met Gly Val Leu Ile Asp Ile Val Pro Asn His Val Gly Val Ala
 85 90 95
 ACG CCG GCG CAG AAC CCC TGG TGG TCG CTG CTC AAG GAG GGA CGC 1013
 50 Thr Pro Ala Gln Asn Pro Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg
 100 105 110

5 CAG TCC CGT TAC GCG GAG GCG TTC GAC GTC GAT TGG GAC CTC GCC GGG 1061
 Gln Ser Arg Tyr Ala Glu Ala Phe Asp Val Asp Trp Asp Leu Ala Gly
 115 120 125
 10 GGA CGC ATC CGG CTG CCG GTG CTC GGC AGC GAC GAT GAC CTC GAC CAG 1109
 Gly Arg Ile Arg Leu Pro Val Leu Gly Ser Asp Asp Asp Leu Asp Gln
 130 135 140
 15 CTC GAA ATC AGG GAC GGG GAG CTG CGG TAC TAC GAC CAC CGA TTC CCG 1157
 Leu Glu Ile Arg Asp Gly Glu Leu Arg Tyr Tyr Asp His Arg Phe Pro
 145 150 155 160
 20 CTC GCC GAG GGA ACC TAC GCC GAA GGC GAC GCC CCG CGG GAT GTC CAC 1205
 Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp Ala Pro Arg Asp Val His
 165 170 175
 25 GCC CGG CAG CAC TAC GAG CTC ATC GGC TGG CGC CGC GCG GAC AAC GAG 1253
 Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg Arg Ala Asp Asn Glu
 180 185 190
 30 CTG AAC TAC CGC CGC TTT TTC GCG GTG AAC ACG CTC GCC GGC GTC CGC 1301
 Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala Gly Val Arg
 195 200 205
 35 GTG GAA ATC CCC GCC GTC TTC GAC GAG GCA CAC CAG GAG GTG GTG CGC 1349
 Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu Val Val Arg
 210 215 220
 40 TGG TTC CGC GAG GAC CTT GCG GAC GGC CTG CGG ATC GAC CAC CCG GAC 1397
 Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His Pro Asp
 225 230 235 240
 45 GGC CTC GCT GAC CCC GAG GGG TAC CTG AAG CGA CTC CGG GAA GTC ACC 1445
 Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val Thr
 245 250 255
 50 GGC GGC GCT TAC CTG CTG ATC GAA AAG ATC CTG GAG CCG GGG GAG CAG 1493
 Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln

5	260	265	270
	CTG CCC GCC AGC TTC GAG TGT GAA GGC ACC ACA GCA GGC TAC GAC GCC CTC 1541		
	Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu		
10	275	280	285
	GCC GAC GTC GAC CGG GTT CTC GTG GAC CCG CGC GGC CAG GAA CCG CTG 1589		
	Ala Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu		
15	290	295	300
	GAC CGG CTT GAC GCG TCC CTG CGT GGC GGC GAG CCC GCC GAC TAC CAG 1637		
	Asp Arg Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln		
20	305	310	315
	GAC ATG ATC CGC GGA ACC AAG CGC CGG ATC ACC GAC GGT ATC CTG CAC 1685		
	Asp Met Ile Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His		
25	325	330	335
	TCG GAG ATC CTG CGG CTG GCC CGG CTG GTT CCG GGC GAC GCC AAC GTT 1733		
	Ser Glu Ile Leu Arg Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val		
30	340	345	350
	TCA ATC GAC GCC GGA GCC GAC GCT CTC GCC GAA ATC ATC GCC GCC TTC 1781		
	Ser Ile Asp Ala Gly Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe		
35	355	360	365
	CCG GTC TAC CGC ACC TAC CTG CCG GAG GGC GCC GAG GTC CTG AAG GAG 1829		
	Pro Val Tyr Arg Thr Tyr Leu Pro Glu Gly Ala Glu Val Leu Lys Glu		
40	370	375	380
	GCG TGC GAG CTT GCC GCG CGT AGG CGG CCG GAA CTC GAC CAG GCC ATC 1877		
	Ala Cys Glu Leu Ala Ala Arg Arg Pro Glu Leu Asp Gln Ala Ile		
45	385	390	395
	CAG GCT CTG CAG CCG CTG CTG GAC ACG GAC CTC GAG CTT GCC CGG 1925		
	Gln Ala Leu Gln Pro Leu Leu Leu Asp Thr Asp Leu Glu Leu Ala Arg		
50	405	410	415
	CGC TTC CAG CAG ACC TCG GGC ATG GTC ATG GCC AAG GGC GTG GAG GAC 1973		

5 Arg Phe Gln Gln Thr Ser Gly Met Val Met Ala Lys Gly Val Glu Asp
 420 425 430
 ACC GCG TTC TTC CGC TAC AAC CGC CTG GGC ACC CTC ACG GAA GTG GGC 2021
 10 Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly Thr Leu Thr Glu Val Gly
 435 440 445
 GCC GAC CCC ACC GAG TTC GCC GTG GAG CCG GAC GAG TTC CAC GCC CGG 2069
 15 Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp Glu Phe His Ala Arg
 450 455 460
 CTG GCA CGC CGG CAG GCC GAG CTT CCG CTG TCC ATG ACG ACG CTG AGC 2117
 20 Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met Thr Thr Leu Ser
 465 470 475 480
 ACG CAC GAC ACC AAG CGC AGC GAG GAC ACC CGA GCA AGG ATT TCG GTC 2165
 25 Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Ser Val
 485 490 495
 ATT TCC GAG GTT GCG GGT GAC TGG GAA AAG GCC TTG AAC CGG CTG CGC 2213
 30 Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg Leu Arg
 500 505 510
 GAC CTG GCC CCG CTG CCG GAC GGC CCG CTG TCC GCG CTG CTC TGG CAG 2261
 35 Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp Gln
 515 520 525
 GCC ATT GCC GGC GCC TGG CCC GCC AGC CGG GAA CGC CTG CAG TAC TAC 2309
 40 Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 530 535 540
 GCG CTG AAG GCC GCG CGT GAA GCG GGG AAC TCG ACC AAC TGG ACC GAT 2357
 45 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp
 545 550 555 560
 CCG GCC CCC GCG TTC GAG GAG AAG CTG AAG GCC GCG GTC GAC GCC GTG 2405
 50 Pro Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val
 565 570 575

5 TTC GAC AAT CCC GCC GTG CAG GCC GAG GTG GAA GCC CTC GTC GAG CTC 2453
 Phe Asp Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu
 580 585 590
 10 CTG GAG CCG TAC GGA GCT TCG AAC TCC CTC GCC GGC AAG CTC GTG CAG 2501
 Leu Glu Pro Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln
 595 600 605
 15 CTG ACC ATG CCC GGC GTC CCG GAC GTC TAC CAG GGC ACG GAG TTC TGG 2549
 Leu Thr Met Pro Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp
 610 615 620
 20 GAC CGG TCG CTG ACG GAC CCG GAC AAC CGG CGG CCG TTC AGC TTC GAC 2597
 Asp Arg Ser Leu Thr Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp
 625 630 635 640
 25 GAC CGC CGC GCC GCG CTG GAG CAG CTG GAT GCC GGC GAC CTT CCC GCG 2645
 Asp Arg Arg Ala Ala Leu Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala
 645 650 655
 30 TCA TTT ACC GAT GAG CGG ACG AAG CTG CTA GTG ACG TCG CGC GCG CTG 2693
 Ser Phe Thr Asp Glu Arg Thr Lys Leu Leu Val Thr Ser Arg Ala Leu
 660 665 670
 35 CGG CTG CGC CGG GAC CGT CCG GAG CTG TTC ACG GGG TAC CGG CCG GTC 2741
 Arg Leu Arg Arg Asp Arg Pro Glu Leu Phe Thr Gly Tyr Arg Pro Val
 675 680 685
 40 CTG GCC AGC GGG CCC GCC GCC GGG CAC CTG CTC GCG TTC GAC CGC GGC 2789
 Leu Ala Ser Gly Pro Ala Ala Gly His Leu Leu Ala Phe Asp Arg Gly
 690 695 700
 45 ACC GCG GCG GCG CCG GGT GCA TTG ACC CTC GCC ACG CGG CTT CCC TAC 2837
 Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu Ala Thr Arg Leu Pro Tyr
 705 710 715 720
 50 GGG CTG GAA CAG TCG GGT GGA TGG CGG GAC ACC GCC GTC GAA CTT AAC 2885
 Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu Leu Asn

725	730	735
5 ACC GCC ATG AAA GAC GAA CTG ACC GGT GCC GGC TTC GGA CCG GGG GCA		2933
Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe Gly Pro Gly Ala		
740	745	750
10 GTG AAG ATC GCC GAC ATC TTC CGG TCG TTC CCC GTT GCG CTG CTG GTG		2981
Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala Leu Leu Val		
755	760	765
15 CCG CAG ACA GGA GGA GAG TCA		3002
Pro Gln Thr Gly Gly Glu Ser		
770	775	
20 TGACGCACAC CTACCCGGCGG GAAGCCGCGA AACCCGT CCT GGGCCCCGCA CGCTACGACG		3062
TCTGGGCGCC C		
		3073

- 25 35. The process as claimed in 28, wherein said DNA is derived from a microorganism selected from the group consisting of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium*, *Flavobacterium*, *Micrococcus*, *Curto-bacterium*, *Mycobacterium* and *Terrabacter*.
- 30 36. The process as claimed in claim 28, wherein said host is a microorganism of the species *Escherichia coli*.
37. The process as claimed in claim 28, wherein said self-replicable vector is plasmid vector Bluescript II SK(+).
- 35 38. The process as claimed in claim 28, wherein said transformant is inoculated into a liquid culture medium having a pH of 2-8, and cultured at a temperature of 25-65°C for 1-6 days.
39. The process as claimed in claim 28, wherein said recombinant enzyme in the culture is collected by one or more methods selected from the group consisting of centrifugation, filtration, concentration, salting out, dialysis, ion-exchange chromatography, gel filtration chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectrophoresis.
- 40 40. A method to convert a reducing amylaceous saccharide, which contains a step of allowing the recombinant enzyme of claim 25 to act on a reducing amylaceous saccharide having a degree of glucose polymerization of 3 or higher to form a non-reducing saccharide having trehalose structure as an end unit from the amylaceous saccharide.
41. The method as claimed in claim 40, wherein said recombinant enzyme has the following physicochemical properties:
- 50 (1) Molecular weight
About 76,000-87,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE); and
(2) Isoelectric point (pI)
About 3.6-4.6 on isoelectrophoresis.
- 55 42. The method as claimed in claim 40, wherein said recombinant enzyme has an amino acid sequence selected from the group consisting of those as shown in the following SEQ ID NOs:2 and 4 that initiate from the N-terminal, and homologous amino acid sequences to these amino acid sequences:

SEQ ID NO:2

Met Arg Thr Pro Ala Ser Thr Tyr Arg Leu Gln Ile Arg Arg Gly Phe Thr

5

1 5 10 15

Leu Phe Asp Ala Ala Glu Thr Val Pro Tyr Leu Lys Ser Leu Gly Val Asp

20 25 30

10

Trp Ile Tyr Leu Ser Pro Ile Leu Lys Ala Glu Ser Gly Ser Asp His Gly

35 40 45 50

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5 Tyr Asp Val Thr Asp Pro Ala Val Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Gly Ala Gly Met Gly Val Leu
 10 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Ser Pro Pro Gln Asn Pro
 90 95 100
 15 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gly Ser Pro Tyr Ala Val Ala
 105 110 115
 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Ile Pro Val Leu
 20 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Lys Asp Gly Glu Leu Arg
 140 145 150
 25 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Ser Tyr Arg Asp Gly Asp
 155 160 165 170
 Ser Pro Gln Asp Val His Gly Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 30 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 190 195 200
 35 Ala Gly Ile Arg Val Glu Val Pro Pro Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 Val Val Arg Trp Phe Arg Ala Gly Leu Ala Asp Gly Leu Arg Ile Asp His
 40 225 230 235
 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 45 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 50 275 280 285
 Asp Val Asp Arg Val Phe Val Asp Pro Arg Gly Gln Val Pro Leu Asp Arg

5	290	295	300	305
	Leu Asp Ala Arg Leu Arg Gly Gly Ala Pro Ala Asp Tyr Glu Asp Met Ile			
	310	315	320	
10	Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu			
	325	330	335	340
	Arg Leu Ala Arg Leu Val Pro Glu Gln Thr Gly Ile Pro Gly Glu Ala Ala			
15	345	350	355	
	Ala Asp Ala Ile Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Ser Tyr			
	360	365	370	
20	Leu Pro Glu Gly Ala Glu Ile Leu Lys Glu Ala Cys Asp Leu Ala Ala Arg			
	375	380	385	390
	Arg Arg Pro Glu Leu Gly Gln Thr Val Gln Leu Leu Gln Pro Leu Leu Leu			
25	395	400	405	
	Asp Thr Asp Leu Glu Ile Ser Arg Arg Phe Gln Gln Thr Ser Gly Met Val			
	410	415	420	425
30	Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly			
	430	435	440	
	Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ser Leu Glu Pro Glu			
35	445	450	455	
	Glu Phe His Val Arg Met Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met			
	460	465	470	475
40	Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg			
	480	485	490	
	Ile Ser Val Ile Ala Glu Val Ala Pro Glu Trp Glu Lys Ala Leu Asp Arg			
45	495	500	505	510
	Leu Asn Thr Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Thr Leu Leu Trp			
	515	520	525	
50	Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Ser Tyr			
	530	535	540	

5 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Ser Trp Thr Asp Pro
 545 550 555 560
 Asp Pro Ala Phe Glu Glu Ala Leu Ser Ala Val Val Asp Ser Ala Phe Asp
 10 565 570 575
 Asn Pro Glu Val Arg Ala Glu Leu Glu Ala Leu Val Gly Leu Leu Ala Pro
 580 585 590 595
 15 His Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 20 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Ala Glu Arg Ile Arg Ala Leu
 630 635 640 645
 25 Asp Gln Leu Asp Ala Gly His Arg Pro Asp Ser Phe Gln Asp Glu Ala Val
 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Arg Asn Arg Pro Glu
 30 665 670 675 680
 Leu Phe Thr Gly Tyr Arg Pro Val His Ala Arg Gly Pro Ala Ala Gly His
 685 690 695
 35 Leu Val Ala Phe Asp Arg Gly Ala Gly Val Leu Ala Leu Ala Thr Arg
 700 705 710
 Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr Ala Val Glu
 40 715 720 725 730
 Leu Glu Ala Ala Met Thr Asp Glu Leu Thr Gly Ser Thr Phe Gly Pro Gly
 735 740 745
 45 Pro Ala Ala Leu Ser Glu Val Phe Arg Ala Tyr Pro Val Ala Leu Leu Val
 750 755 760 765
 50 Pro Ala Thr Gly Gly Lys Ser
 770

5 SEQ ID NO:4

Met Arg Thr Pro Val Ser Thr Tyr Arg Leu Gln Ile Arg Lys Gly Phe Thr
 1 5 10 15
 10 Leu Phe Asp Ala Ala Lys Thr Val Pro Tyr Leu His Ser Leu Gly Val Asp
 20 25 30
 Trp Val Tyr Leu Ser Pro Val Leu Thr Ala Glu Gln Gly Ser Asp His Gly
 15 35 40 45 50
 Tyr Asp Val Thr Asp Pro Ser Ala Val Asp Pro Glu Arg Gly Gly Pro Glu
 55 60 65
 20 Gly Leu Ala Ala Val Ser Lys Ala Ala Arg Ala Ala Gly Met Gly Val Leu
 70 75 80 85
 Ile Asp Ile Val Pro Asn His Val Gly Val Ala Thr Pro Ala Gln Asn Pro
 25 90 95 100
 Trp Trp Trp Ser Leu Leu Lys Glu Gly Arg Gln Ser Arg Tyr Ala Glu Ala
 105 110 115
 30 Phe Asp Val Asp Trp Asp Leu Ala Gly Gly Arg Ile Arg Leu Pro Val Leu
 120 125 130 135
 Gly Ser Asp Asp Asp Leu Asp Gln Leu Glu Ile Arg Asp Gly Glu Leu Arg
 35 140 145 150
 Tyr Tyr Asp His Arg Phe Pro Leu Ala Glu Gly Thr Tyr Ala Glu Gly Asp
 155 160 165 170
 40 Ala Pro Arg Asp Val His Ala Arg Gln His Tyr Glu Leu Ile Gly Trp Arg
 175 180 185
 Arg Ala Asp Asn Glu Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu
 45 190 195 200
 Ala Gly Val Arg Val Glu Ile Pro Ala Val Phe Asp Glu Ala His Gln Glu
 205 210 215 220
 50 Val Val Arg Trp Phe Arg Glu Asp Leu Ala Asp Gly Leu Arg Ile Asp His
 225 230 235

5 Pro Asp Gly Leu Ala Asp Pro Glu Gly Tyr Leu Lys Arg Leu Arg Glu Val
 240 245 250 255
 10 Thr Gly Gly Ala Tyr Leu Leu Ile Glu Lys Ile Leu Glu Pro Gly Glu Gln
 260 265 270
 15 Leu Pro Ala Ser Phe Glu Cys Glu Gly Thr Thr Gly Tyr Asp Ala Leu Ala
 275 280 285
 20 Asp Val Asp Arg Val Leu Val Asp Pro Arg Gly Gln Glu Pro Leu Asp Arg
 290 295 300 305
 25 Leu Asp Ala Ser Leu Arg Gly Gly Glu Pro Ala Asp Tyr Gln Asp Met Ile
 310 315 320
 30 Arg Gly Thr Lys Arg Arg Ile Thr Asp Gly Ile Leu His Ser Glu Ile Leu
 325 330 335 340
 35 Asp Leu Ala Arg Leu Val Pro Gly Asp Ala Asn Val Ser Ile Asp Ala Gly
 345 350 355
 40 Ala Asp Ala Leu Ala Glu Ile Ile Ala Ala Phe Pro Val Tyr Arg Thr Tyr
 360 365 370
 45 Leu Pro Glu Gly Ala Glu Val Leu Lys Glu Ala Cys Glu Leu Ala Ala Arg
 375 380 385 390
 50 Arg Arg Pro Glu Leu Asp Gln Ala Ile Gln Ala Leu Gln Pro Leu Leu
 395 400 405
 55 Asp Thr Asp Leu Glu Leu Ala Arg Arg Phe Gln Gln Thr Ser Gly Met Val
 410 415 420 425
 Met Ala Lys Gly Val Glu Asp Thr Ala Phe Phe Arg Tyr Asn Arg Leu Gly
 430 435 440
 Thr Leu Thr Glu Val Gly Ala Asp Pro Thr Glu Phe Ala Val Glu Pro Asp
 445 450 455
 55 Glu Phe His Ala Arg Leu Ala Arg Arg Gln Ala Glu Leu Pro Leu Ser Met
 460 465 470 475
 Thr Thr Leu Ser Thr His Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg

5 480 485 490
 Ile Ser Val Ile Ser Glu Val Ala Gly Asp Trp Glu Lys Ala Leu Asn Arg
 495 500 505 510
 10 Leu Arg Asp Leu Ala Pro Leu Pro Asp Gly Pro Leu Ser Ala Leu Leu Trp
 515 520 525
 Gln Ala Ile Ala Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Gln Tyr Tyr
 15 530 535 540
 Ala Leu Lys Ala Ala Arg Glu Ala Gly Asn Ser Thr Asn Trp Thr Asp Pro
 20 545 550 555 560
 Ala Pro Ala Phe Glu Glu Lys Leu Lys Ala Ala Val Asp Ala Val Phe Asp
 565 570 575
 Asn Pro Ala Val Gln Ala Glu Val Glu Ala Leu Val Glu Leu Leu Glu Pro
 25 580 585 590 595
 Tyr Gly Ala Ser Asn Ser Leu Ala Ala Lys Leu Val Gln Leu Thr Met Pro
 30 600 605 610
 Gly Val Pro Asp Val Tyr Gln Gly Thr Glu Phe Trp Asp Arg Ser Leu Thr
 615 620 625
 Asp Pro Asp Asn Arg Arg Pro Phe Ser Phe Asp Asp Arg Arg Ala Ala Leu
 35 630 635 640 645
 Glu Gln Leu Asp Ala Gly Asp Leu Pro Ala Ser Phe Thr Asp Glu Arg Thr
 40 650 655 660
 Lys Leu Leu Val Thr Ser Arg Ala Leu Arg Leu Arg Asp Arg Pro Glu
 665 670 675 680
 45 Leu Phe Thr Gly Tyr Arg Pro Val Leu Ala Ser Gly Pro Ala Ala Gly His
 685 690 695
 Leu Leu Ala Phe Asp Arg Gly Thr Ala Ala Ala Pro Gly Ala Leu Thr Leu
 50 700 705 710
 Ala Thr Arg Leu Pro Tyr Gly Leu Glu Gln Ser Gly Gly Trp Arg Asp Thr
 715 720 725 730
 55

Ala Val Glu Leu Asn Thr Ala Met Lys Asp Glu Leu Thr Gly Ala Gly Phe

735 740

745

Gly Pro Gly Ala Val Lys Ile Ala Asp Ile Phe Arg Ser Phe Pro Val Ala

750 755 760 765

Leu Leu Val Pro Gln Thr Gly Gly Glu Ser

770 775

43. The method as claimed in claim 40, wherein said reducing amyloseous saccharide is a member selected
15 from the group consisting of starch hydrolysate and amyloseous substance which has been treated with
acid together with or without amylase.

44. The method as claimed in claim 40, wherein said reducing amyloseous saccharide is a member selected
20 from the group consisting of maltotriose, maltotetraose, maltopentaose, maltohexaose, maltoheptaose
and mixtures thereof.

45. The method as claimed in claim 40, wherein the reducing amyloseous saccharide is in a solution form
with a concentration of 50 w/v % or lower, and the step is carried out at a temperature of 40-55°C and a
pH of 5-10.

25 46. The method as claimed in claim 40, wherein said non-reducing saccharide is a member selected from
the group of consisting of α -glucosyl trehalose, α -maltosyl trehalose, α -maltotriosyl trehalose, α -malo-
tetraosyl trehalose, α -maltopentaosyl trehalose, and mixtures thereof.

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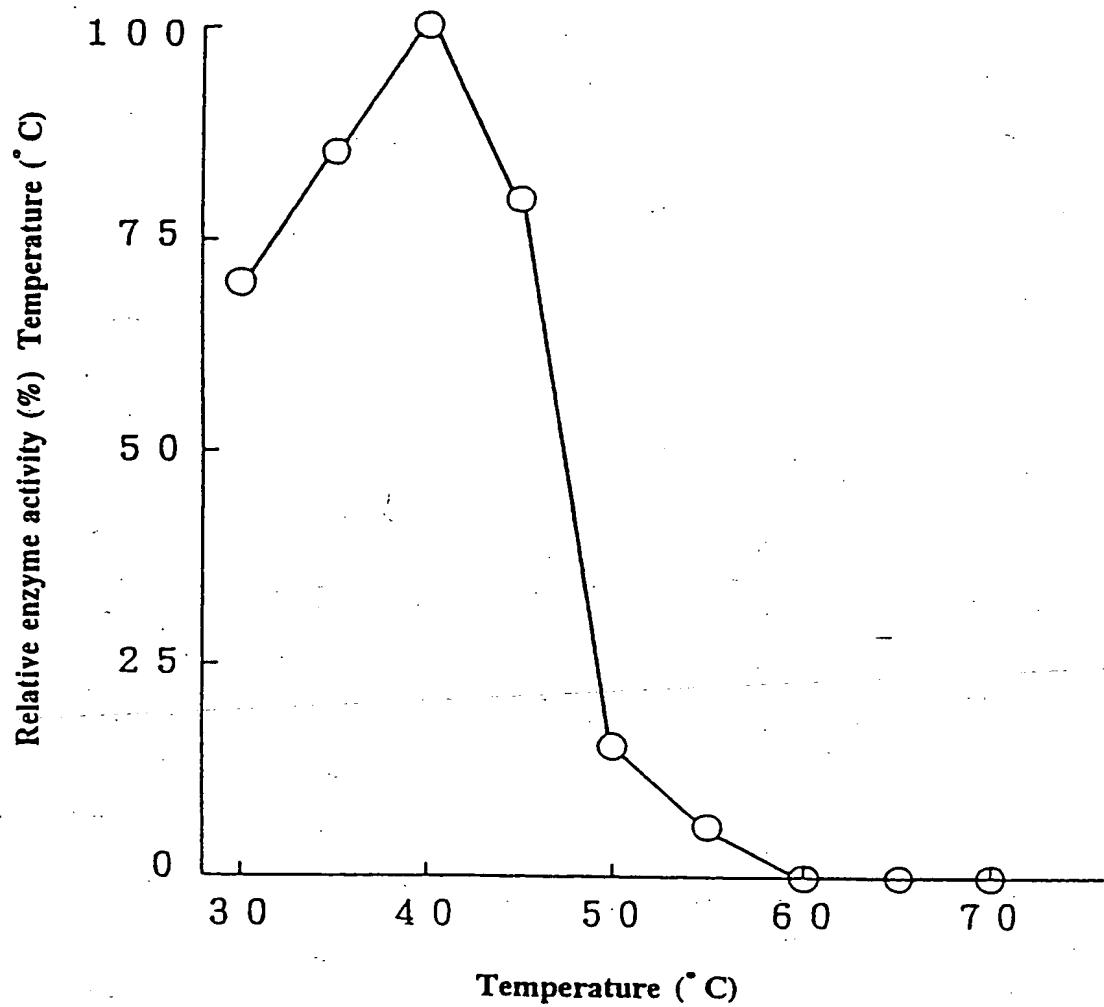


FIG. 1

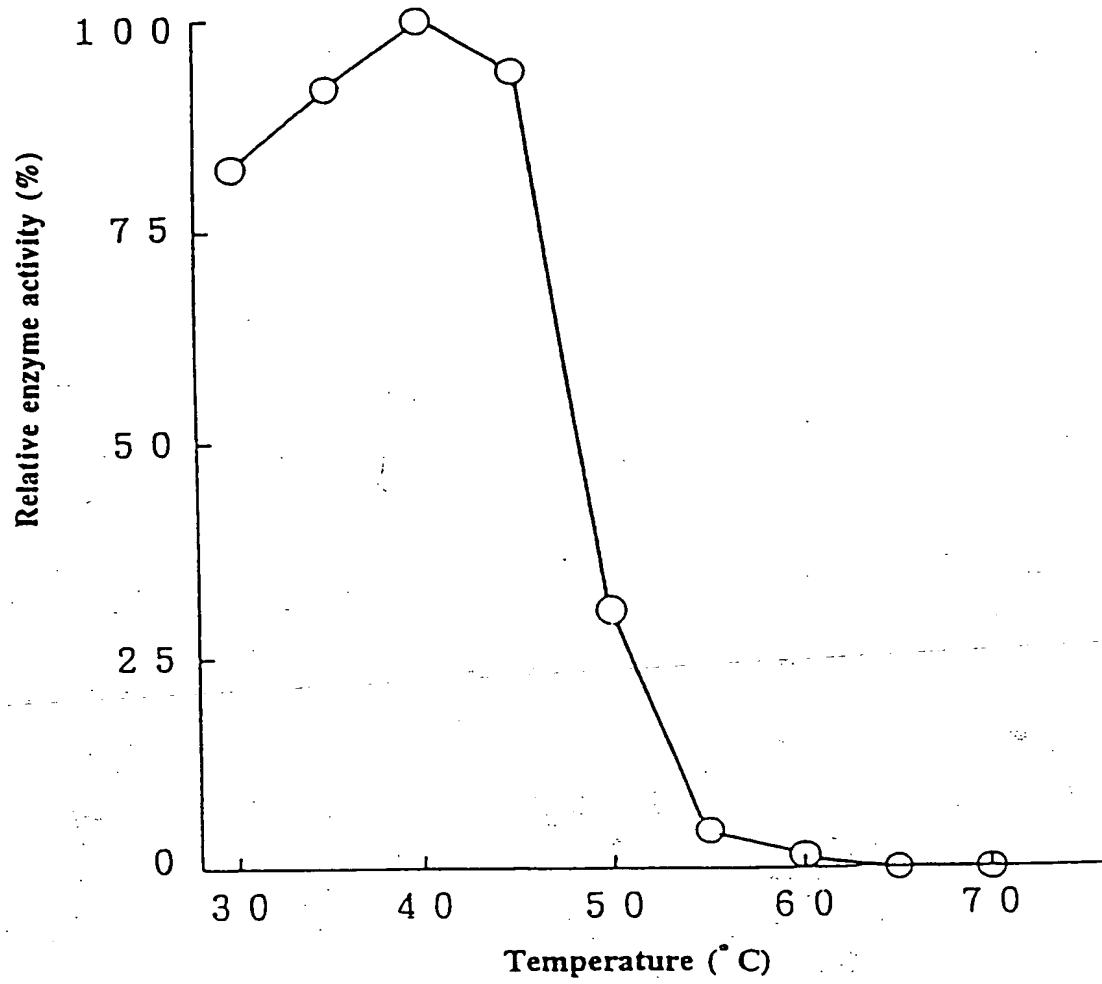


FIG. 2

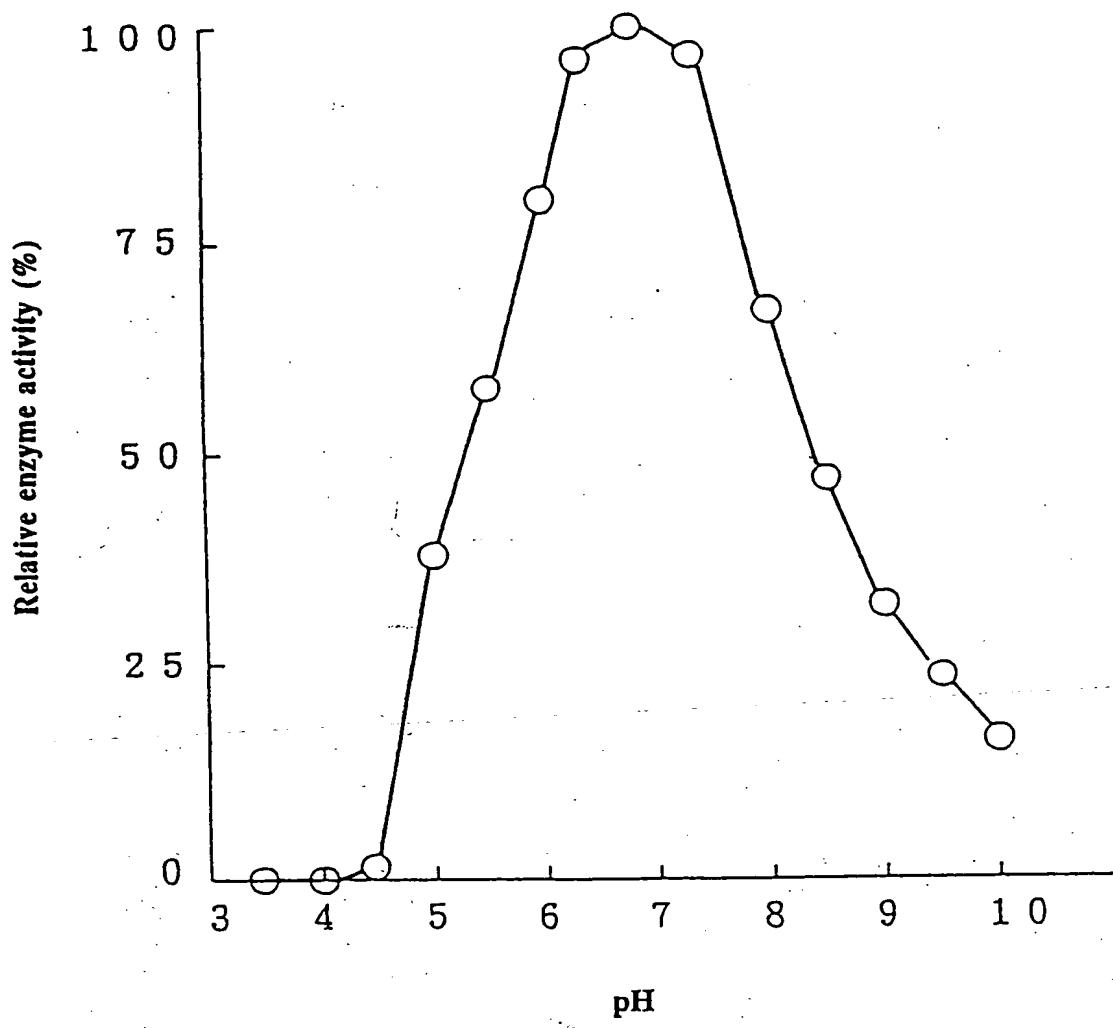


FIG. 3

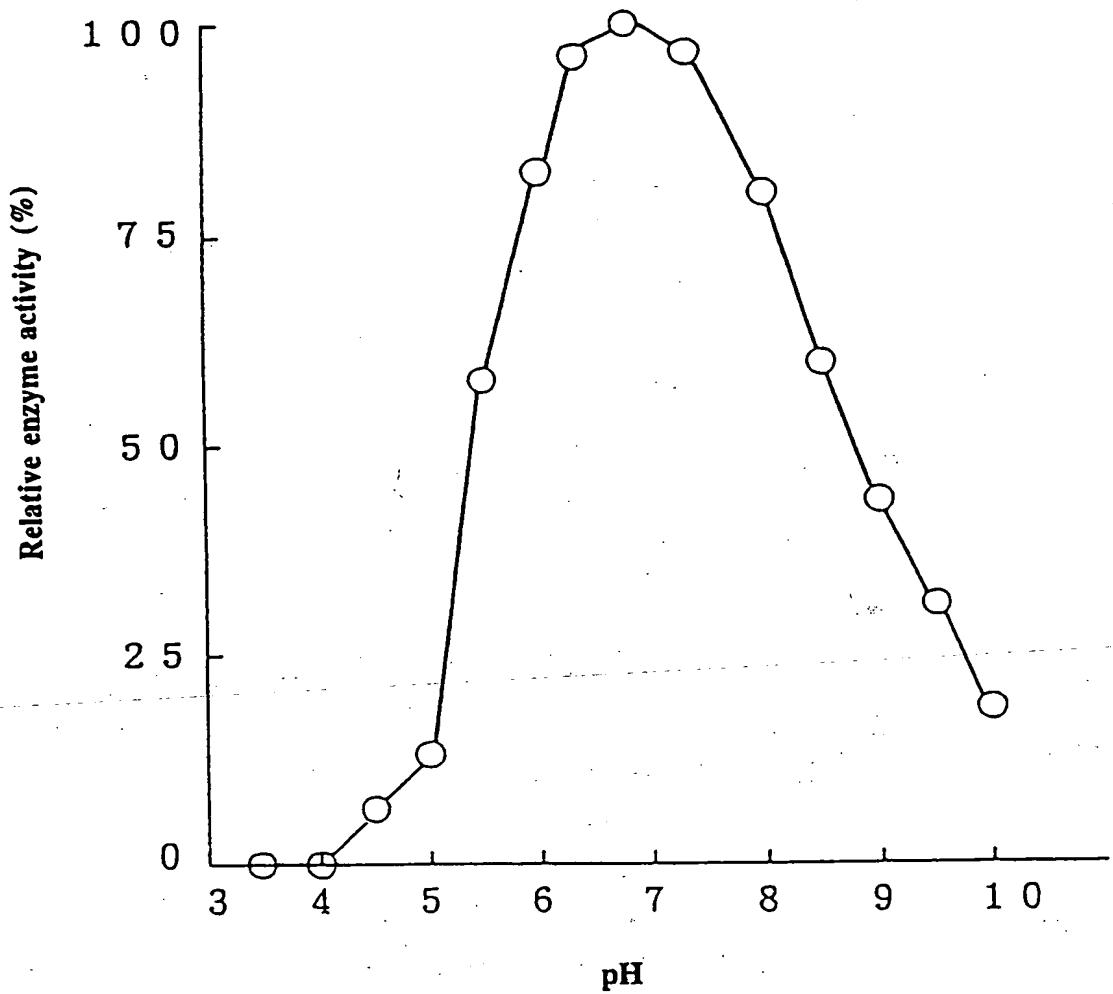


FIG. 4

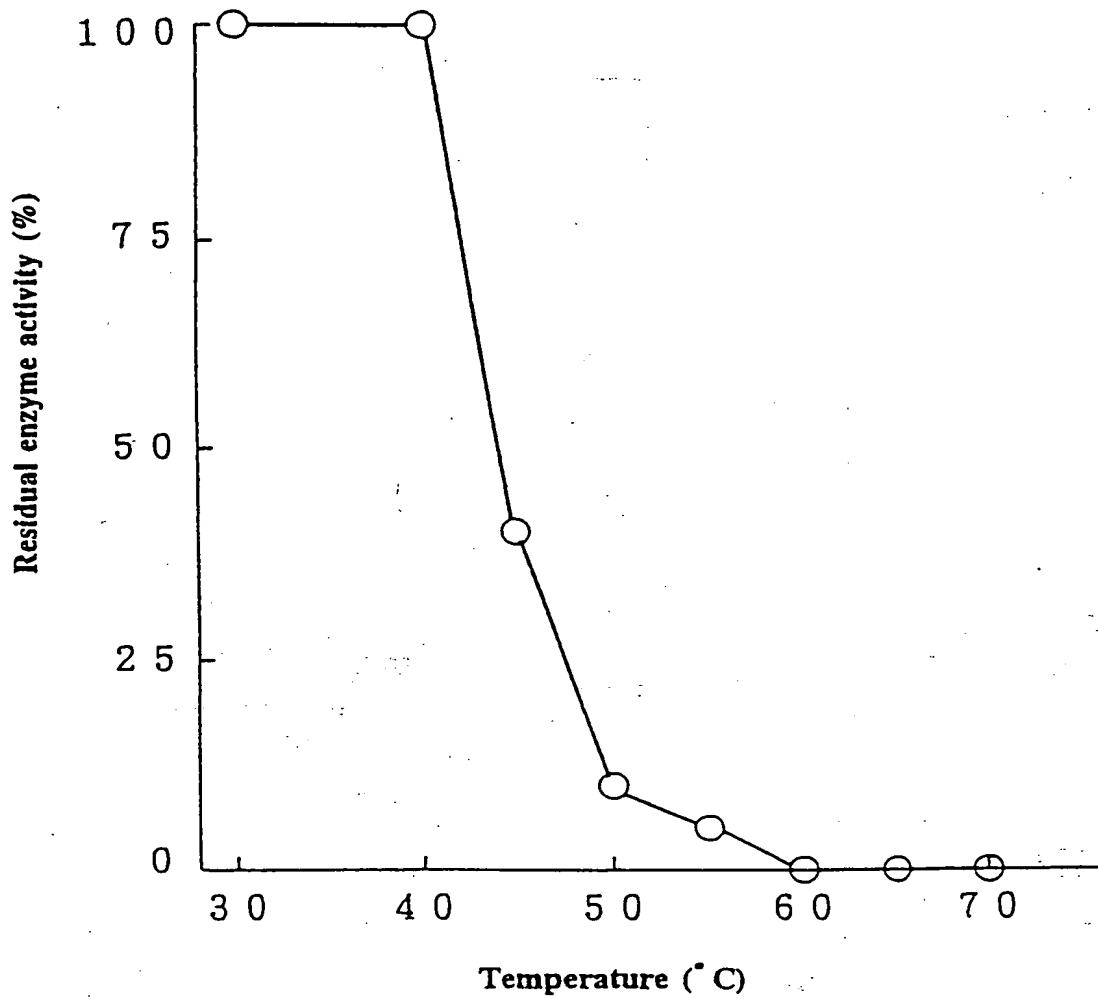


FIG. 5

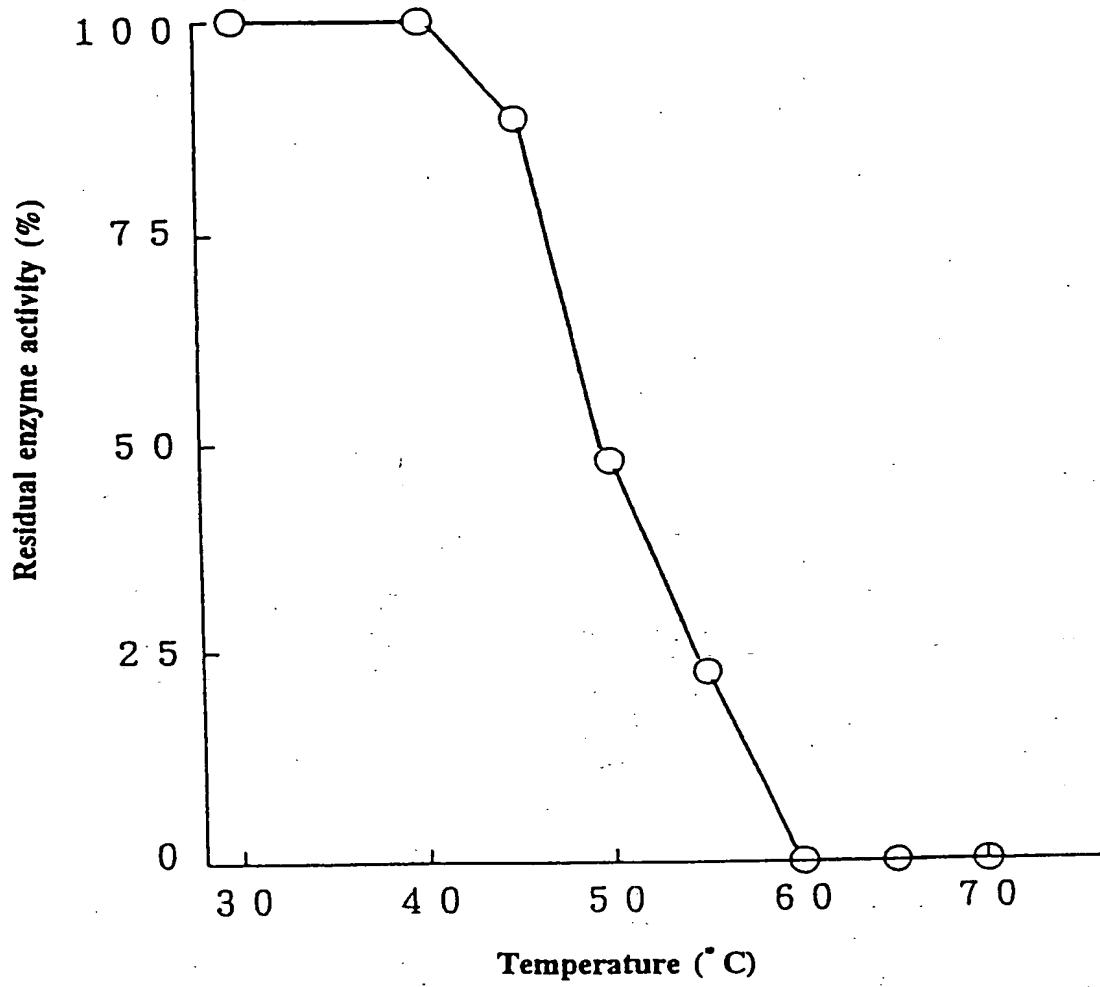


FIG. 6

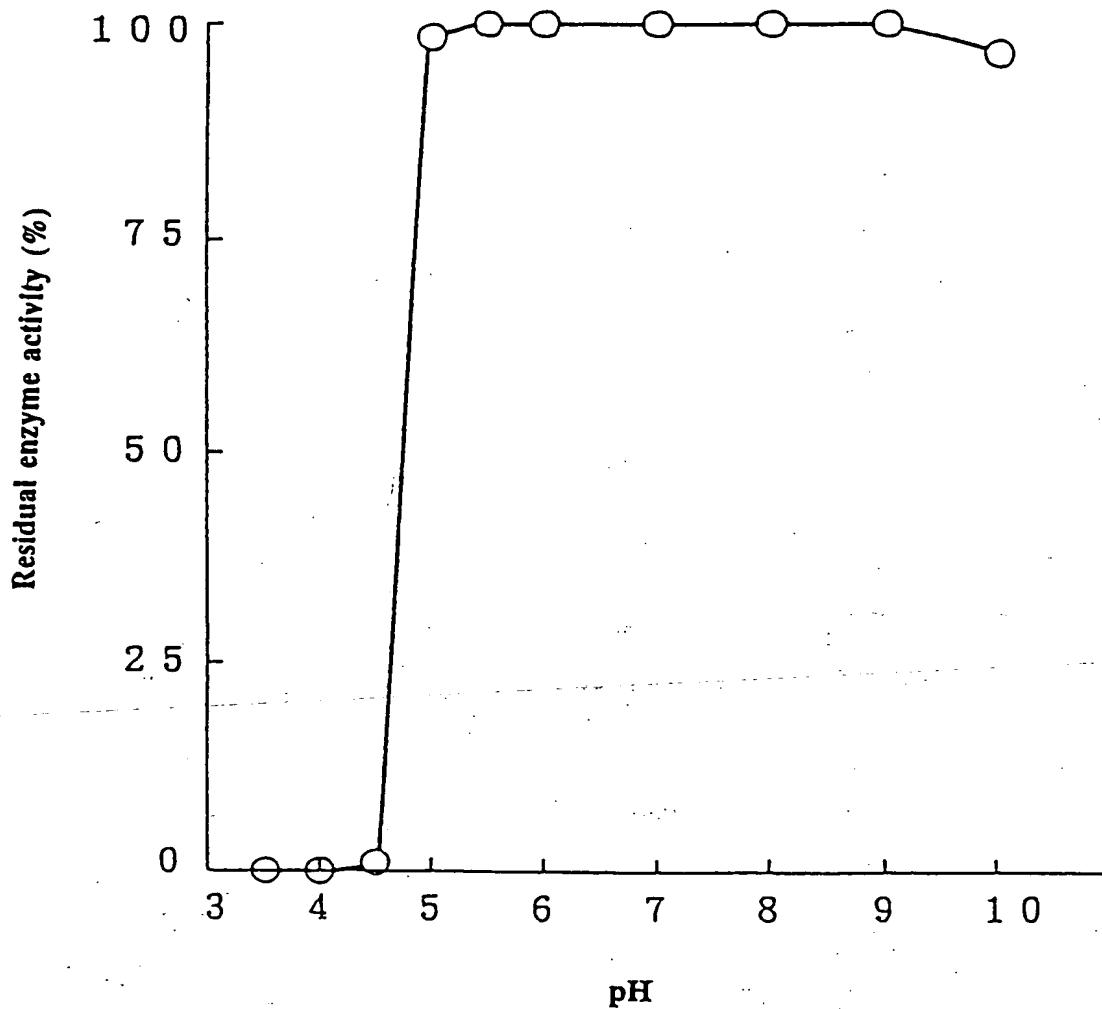


FIG. 7

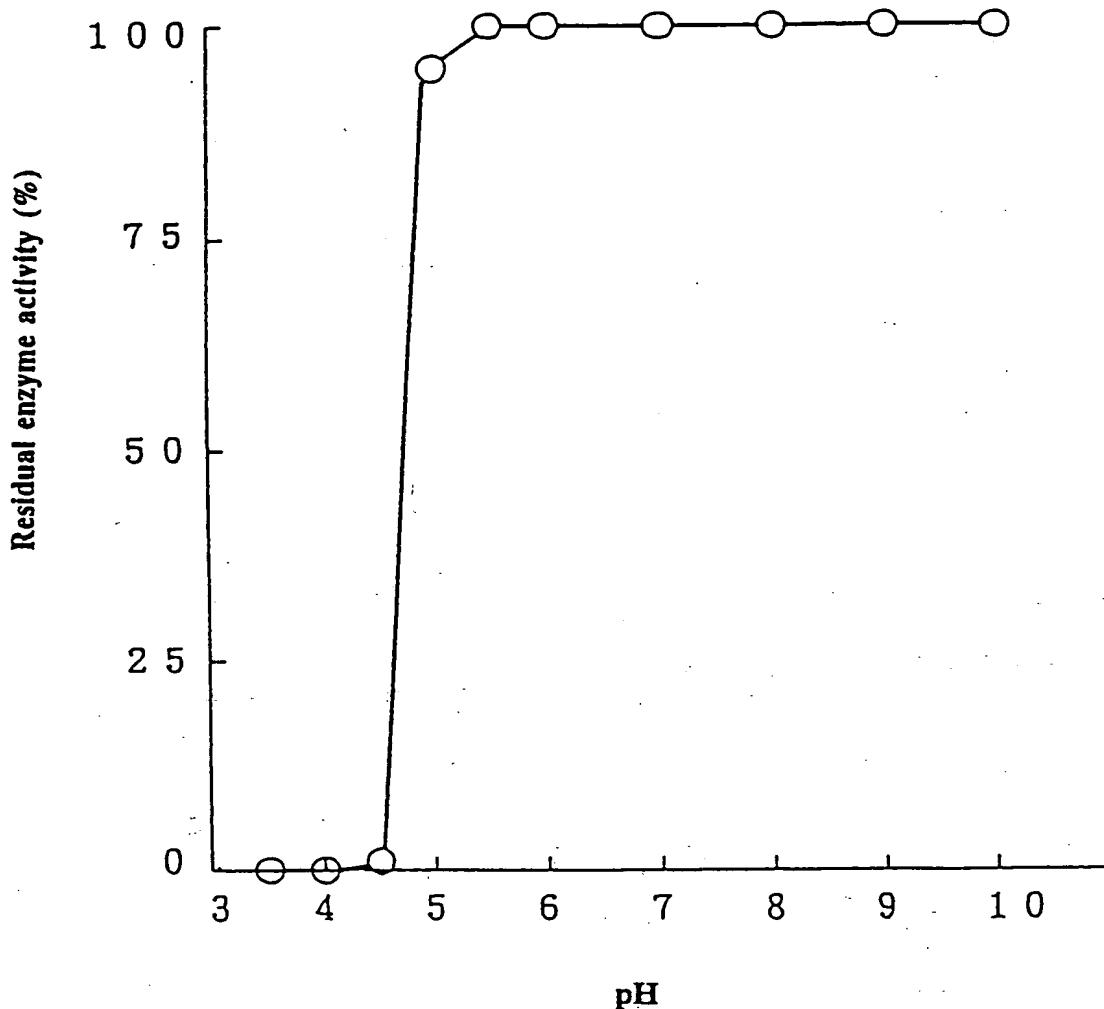


FIG. 8

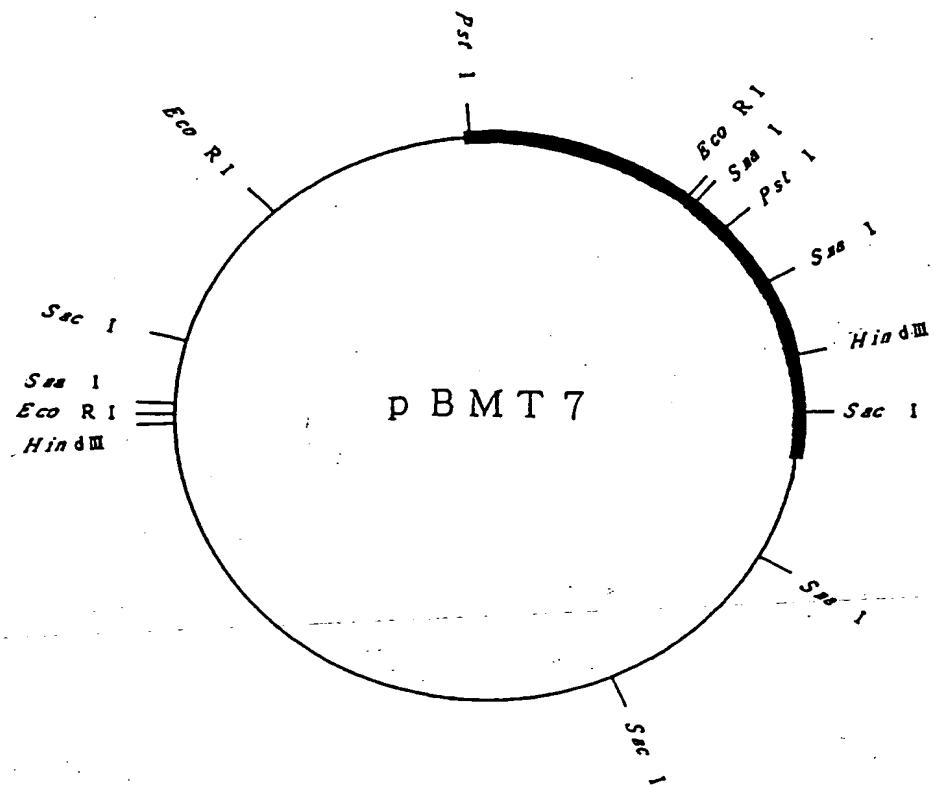


FIG. 9

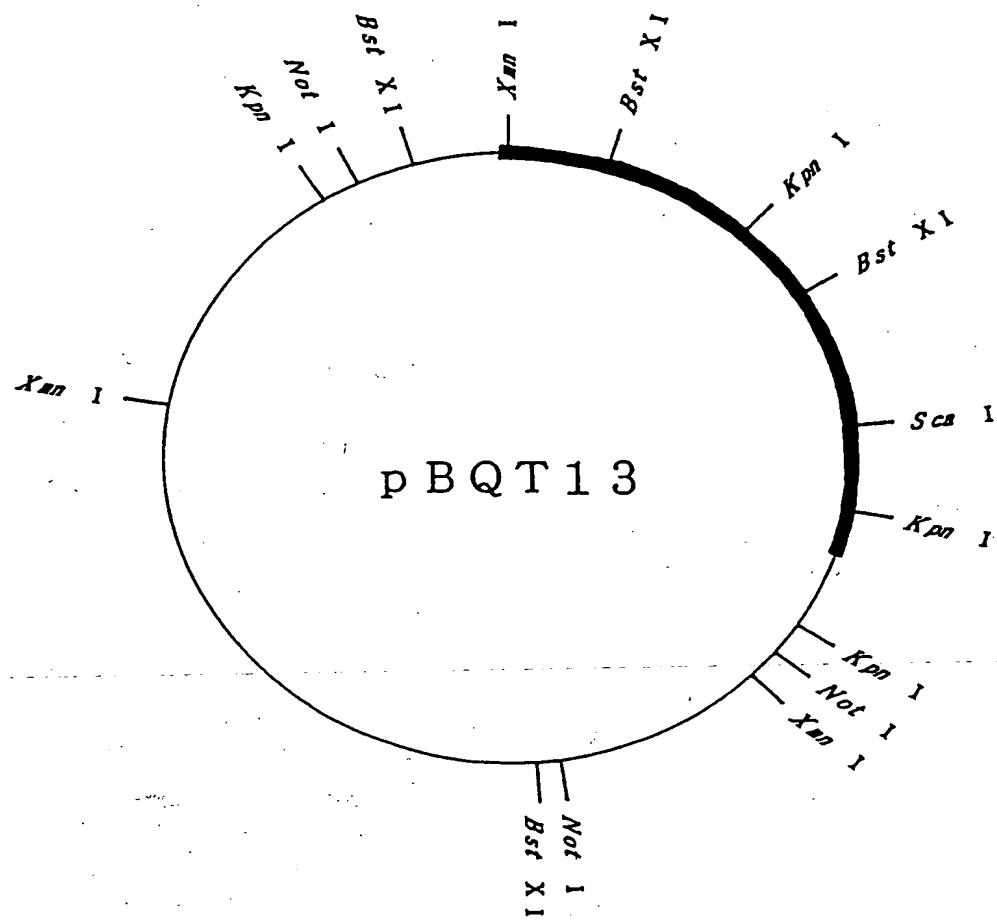


FIG. 10